

GenCore version 4.5
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OM nucleic - nucleic search, using SW model

```
Run on:      December 3, 2000, 19:31:01 ; Search time 727.75 seconds
              (without alignments)
              2720.877 Million cell updates/sec
```

```

Title: US-09-227-881-34
Perfect score: 5271
Sequence: 1 abcttgtcagtttacc...tcggcatgagccagcaagg 5271

```

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 480022 seqs, 187831343 residues

Total number of hits satisfying chosen parameters: 960044

```
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
```

```
Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries
```

```
Database :
N_Geneseq_36:
1: /cgn2_2/gcgdata/geneseq/genseqn/NA1980.DAT.*
2: /cgn2_2/gcgdata/geneseq/genseqn/NA1981.DAT.*
3: /cgn2_2/gcgdata/geneseq/genseqn/NA1982.DAT.*
4: /cgn2_2/gcgdata/geneseq/genseqn/NA1983.DAT.*
5: /cgn2_2/gcgdata/geneseq/genseqn/NA1984.DAT.*
6: /cgn2_2/gcgdata/geneseq/genseqn/NA1985.DAT.*
7: /cgn2_2/gcgdata/geneseq/genseqn/NA1986.DAT.*
8: /cgn2_2/gcgdata/geneseq/genseqn/NA1987.DAT.*
9: /cgn2_2/gcgdata/geneseq/genseqn/NA1988.DAT.*
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12: /cgn2_2/gcgdata/geneseq/genseqn/NA1991.DAT.*
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18: /cgn2_2/gcgdata/geneseq/genseqn/NA1997.DAT.*
19: /cgn2_2/gcgdata/geneseq/genseqn/NA1998.DAT.*
20: /cgn2_2/gcgdata/geneseq/genseqn/NA1999.DAT.*
21: /cgn2_2/gcgdata/geneseq/genseqn/NA2000.DAT.*
```

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB | ID | Description |
|------------|--------|-------------|--------|----|---------|---------------------|
| 1 | 5271 | 100.0 | 6169 | 19 | V51368 | Human TIGR upstream |
| 2 | 5246.4 | 99.5 | 5299 | 19 | V51361 | Human TIGR promote |
| 3 | 5244.8 | 99.5 | 5300 | 19 | V51362 | Human TIGR promote |
| 4 | 5244.8 | 99.5 | 5300 | 19 | V51363 | Human TIGR promote |
| 5 | 5244.8 | 99.5 | 5300 | 19 | V51365 | Human TIGR promote |
| 6 | 5244.8 | 99.5 | 5300 | 19 | V51366 | Human TIGR promote |
| 7 | 5244.8 | 99.5 | 5300 | 19 | V51367 | Human TIGR promote |
| 8 | 5232.4 | 99.3 | 5304 | 19 | V51364 | Human TIGR promote |
| 9 | 1804.4 | 34.2 | 2800 | 21 | Z37968 | Human GCLC gene e |
| 10 | 176.4 | 3.3 | 283 | 15 | O63862 | AP2 sequence obd. |
| 11 | 175.2 | 3.3 | 162450 | 21 | Z865967 | Retinoldehome bin |
| 12 | 174.2 | 3.3 | 282 | 18 | T63346 | Consensus Alu repe |

| | | | | | | |
|---|----|-------|-----|--------|----|--------|
| C | 13 | 173.6 | 3.3 | 17327 | 14 | 044278 |
| C | 14 | 173.2 | 3.3 | 49999 | 17 | 223900 |
| C | 15 | 172.8 | 3.3 | 452 | 17 | T42809 |
| C | 16 | 172.8 | 3.3 | 106746 | 21 | A10288 |
| C | 17 | 172 | 3.3 | 2932 | 1 | Q25385 |
| C | 18 | 172 | 3.3 | 2932 | 20 | Z32161 |
| C | 19 | 172 | 3.3 | 2932 | 20 | Z32162 |
| C | 20 | 172 | 3.3 | 43069 | 21 | Z36335 |
| C | 21 | 171.6 | 3.3 | 10380 | 18 | T67164 |
| C | 22 | 171.2 | 3.2 | 21721 | 20 | X83427 |
| C | 23 | 171.2 | 3.2 | 22976 | 20 | X83426 |
| C | 24 | 171 | 3.2 | 54548 | 21 | Z45596 |
| C | 25 | 170.8 | 3.2 | 2617 | 21 | A23452 |
| C | 26 | 170.4 | 3.2 | 3334 | 16 | Q92781 |
| C | 27 | 170 | 3.2 | 15056 | 19 | Y52967 |
| C | 28 | 170 | 3.2 | 15056 | 21 | Z99333 |
| C | 29 | 169.6 | 3.2 | 2426 | 21 | A06689 |
| C | 30 | 169 | 3.2 | 2543 | 18 | T75284 |
| C | 31 | 168.4 | 3.2 | 11788 | 16 | Q90512 |
| C | 32 | 168.2 | 3.2 | 3089 | 21 | Z64938 |
| C | 33 | 167.4 | 3.2 | 555 | 20 | V90098 |
| C | 34 | 167.4 | 3.2 | 41783 | 21 | A35059 |
| C | 35 | 167.4 | 3.2 | 138169 | 21 | A34791 |
| C | 36 | 167.4 | 3.2 | 141589 | 21 | A35005 |
| C | 37 | 167.4 | 3.2 | 141589 | 21 | A35030 |
| C | 38 | 167.4 | 3.2 | 162450 | 21 | Z85967 |
| C | 39 | 166.8 | 3.2 | 7849 | 16 | Q94109 |
| C | 40 | 166.4 | 3.2 | 1601 | 21 | A35131 |
| C | 41 | 166.4 | 3.2 | 1601 | 21 | Z46814 |
| C | 42 | 166.4 | 3.2 | 1618 | 12 | Q10207 |
| C | 43 | 166.4 | 3.2 | 1618 | 14 | Q46958 |
| C | 44 | 166.4 | 3.2 | 1618 | 21 | Z86905 |
| C | 45 | 166.4 | 3.2 | 1645 | 21 | Z58659 |

| | |
|--------|--|
| RESULT | 1 |
| V51368 | ID V51368 standard; DNA; 6169 BP. |
| XX | |
| AC | V51368; |
| XX | |
| DT | 27-OCT-1998 (first entry) |
| XX | |
| DE | Human TIGR upstream region and exon 1 DNA. |
| XX | |
| KW | TIGR: trabecular meshwork induced glucocorticoid response protein; human |
| KM | diagnosis; glaucoma; polymorphism; steroid sensitivity; ss. |
| XX | |
| OS | Homo sapiens. |
| XX | |
| FH | Location/Qualifiers |
| FT | Key |
| FT | exon |
| FT | 5301..5940 |
| FT | /tag= a |
| FT | /number=1 |
| FT | 5337..6169 |
| CDS | |
| FT | /tag= b |
| FT | /product= "TIGR" |
| FT | /note= "partial coding sequence" |
| FT | 5941..6169 |
| FT | /tag= c |
| FT | /number=1 |
| FT | /note= "partial intron sequence" |
| XX | |
| PN | M09832850-A1. |
| XX | |
| PD | 30-JUL-1998. |
| XX | |
| PF | 09-JAN-1998; 98WO-US00468. |
| XX | |
| PR | 26-SEP-1997; 97US-0938669. |

PR 28-JAN-1997: 97US-0791154.
XX
XX (REGC) UNIV CALIFORNIA.
XX
PI Chen H, Chen P, Nguyen TD, Polansky JR:
XX WPI: 1998-427946/36.
XX
XX
PT Use of TIGR nucleic acid sequences - used for, e.g. developing
PI products for diagnosis, prognosis and treatment of glaucoma
XX
XX
PS Claim 37, Fig 3: 105pp: English.
XX
CC This sequence is a trabecular meshwork induced glucocorticoid response
CC protein (TIGR) upstream region and exon 1. This DNA sequence can be used
CC in a method for diagnosing glaucoma in a patient. The method involves the
CC detection of polymorphisms whose presence is predictive of a mutation
CC affecting TIGR response in the patient and can be diagnostic of glaucoma
CC or steroid sensitivity. Base substitutions and base additions upstream of
CC and within TIGR exons can also be used to diagnose glaucoma.
XX
XX
SQ Sequence 6169 BP: 1702 A: 1389 C: 1491 G: 1587 T: 0 other:

Query Match 100.0%; Score 5271; DB 19; Length 6169;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 5271; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 attcttgctcagtttccctccagggccattatgaatagaataaataaataatgaatgaag 60
DB 1 attcttgctcagtttccctccagggccattatgaatagaataaataaataatgaatgaag 60
QY 61 tccataaactgatatgctccatccatcgtatgatacttcttgccagatgataaataca 120
DB 61 tccataaactgatatgctccatccatcgtatgatacttcttgccagatgataaataca 120
QY 121 ggaagaagaagatgccagcttagcagaagtgtccagagctgtcctcttattagtgta 180
DB 121 ggaagaagaagatgccagcttagcagaagtgtccagagctgtcctcttattagtgta 180
QY 181 cagatgtctcctctgacgaagaactctcttcaggaatacaataccaatctgttaactc 240
DB 181 cagatgtctcctctgacgaagaactctcttcaggaatacaataccaatctgttaactc 240
QY 241 catcaaacagagagctaaagaagaatgagatgagcactgcccagaagaataatgccaag 300
DB 241 catcaaacagagagctaaagaagaatgagatgagcactgcccagaagaataatgccaag 300
QY 301 gagagcaataatgatacgaataaataaactcttcctctgttttaatttcaggaataatg 360
DB 301 gagagcaataatgatacgaataaataaactcttcctctgttttaatttcaggaataatg 360
QY 361 atgagagcaataatgatacgaataaataaactcttcctctgttttaatttcaggaataatg 420
DB 361 atgagagcaataatgatacgaataaataaactcttcctctgttttaatttcaggaataatg 420
QY 421 taatttaagtattcttcccttggaagagacccatcgtgagctgatacgtggaataatgga 480
DB 421 taatttaagtattcttcccttggaagagacccatcgtgagctgatacgtggaataatgga 480
QY 481 aaaggtcaaaagcattgatacgaatcccaaatggtatattattttaaaaccagat 540
DB 481 aaaggtcaaaagcattgatacgaatcccaaatggtatattattttaaaaccagat 540
QY 541 ggcatacctcgggagagcagaatccagaagagatgttgcaaaaggacttaacaataac 600
DB 541 ggcatacctcgggagagcagaatccagaagagatgttgcaaaaggacttaacaataac 600
QY 601 agcaaaaatcaaaatcccgcaaatgcaaggagaaatgaggacggaagcttcttaaac 660
DB 601 agcaaaaatcaaaatcccgcaaatgcaaggagaaatgaggacggaagcttcttaaac 660
QY 661 agtgaataggcagtgaacacatgttcgcaaacactcccgctctataccaggaacacaaaa 720

DB 661 agtgaataggcagtgaacacatgttcgcaaacactcccgctctataccaggaacacaaaa 720
QY 721 attgactggtctaaagccctgacattcaagggaataatgaataaactggaagcaaaacaaa 780
DB 721 attgactggtctaaagccctgacattcaagggaataatgaataaactggaagcaaaacaaa 780
QY 781 gacatggttaaaagcagaacaggaacattgtgagcttcaagcagcagctccctcagca 840
DB 781 gacatggttaaaagcagaacaggaacattgtgagcttcaagcagcagctccctcagca 840
QY 841 gggaccctgaggcattgctcctttagaaggccagtttctctaaaggaaatcttaagaactc 900
DB 841 gggaccctgaggcattgctcctttagaaggccagtttctctaaaggaaatcttaagaactc 900
QY 901 ttgaaagctcagatatttaacccctttaaagataaaacaataatgcagatgataatcag 960
DB 901 ttgaaagctcagatatttaacccctttaaagataaaacaataatgcagatgataatcag 960
QY 961 tttagacatggtcccaattttaaagatcagacatacaaggatgaaggtcccaagctcc 1020
DB 961 tttagacatggtcccaattttaaagatcagacatacaaggatgaaggtcccaagctcc 1020
QY 1021 ggaatagctcagaataatcaatgaatacaactgtgtcccatcctaacttttcagaatgac 1080
DB 1021 ggaatagctcagaataatcaatgaatacaactgtgtcccatcctaacttttcagaatgac 1080
QY 1081 tgtcatagccctcaacaacagcccgatgtgtcagctcccaacacacatctcaaacccaa 1140
DB 1081 tgtcatagccctcaacaacagcccgatgtgtcagctcccaacacacatctcaaacccaa 1140
QY 1141 gtgcctcaaacattgtttaaagtgtcattcagtaggtcccatcaacaatgccaactccccc 1200
DB 1141 gtgcctcaaacattgtttaaagtgtcattcagtaggtcccatcaacaatgccaactccccc 1200
QY 1201 tgtgagagccatcccgctcccaaggaagtctcccaactctagaactctgcatcaagatgt 1260
DB 1201 tgtgagagccatcccgctcccaaggaagtctcccaactctagaactctgcatcaagatgt 1260
QY 1261 taacagcagaagaagctccgttagagggtgaggtctgtgtcttaacacacacttgatgtctac 1320
DB 1261 taacagcagaagaagctccgttagagggtgaggtctgtgtcttaacacacacttgatgtctac 1320
QY 1321 accctgagctcaactgcaaacctctgctcccaaggttcaagcaattctcctgctcagcctcc 1380
DB 1321 accctgagctcaactgcaaacctctgctcccaaggttcaagcaattctcctgctcagcctcc 1380
QY 1381 cgcgtagctgggaactcaacagggcgacgcccgcataattttgtatgttagtagatggg 1440
DB 1381 cgcgtagctgggaactcaacagggcgacgcccgcataattttgtatgttagtagatggg 1440
QY 1441 gttccacataatgacccgagctggtctgaactcctctgaccccaaggtatccacacactc 1500
DB 1441 gttccacataatgacccgagctggtctgaactcctctgaccccaaggtatccacacactc 1500
QY 1501 agccctccaaagtgtcgtgattacagatgatacagcgcccgcaagggtcagtggt 1560
DB 1501 agccctccaaagtgtcgtgattacagatgatacagcgcccgcaagggtcagtggt 1560
QY 1561 ttaataaagaataaacttaactgattacttaacccaagaaggaaacagaaagctgtga 1620
DB 1561 ttaataaagaataaacttaactgattacttaacccaagaaggaaacagaaagctgtga 1620
QY 1621 taatttcaggagattcttggaatgggaatggtgtgcatacgtgacgtccctcaggtccagac 1680
DB 1621 taatttcaggagattcttggaatgggaatggtgtgcatacgtgacgtccctcaggtccagac 1680
QY 1681 cactggtctcctaactctctccctcaactcaatttcaggactgaagttaacattat 1740
DB 1681 cactggtctcctaactctctccctcaactcaatttcaggactgaagttaacattat 1740
QY 1741 caccatgctttgtgtaagccttcacatgttactgaataatgaagtatacaataactag 1800

| | | | |
|----|------|---|------|
| Dh | 1741 | caccagctcttctgtgtgaagccctccacacacgcttaccgaaataagsgtataataactag | 1800 |
| Qy | 1801 | tcccatctggsgccatctgtgtgtgtataagsggagsgacabaccacagagactctc | 1860 |
| Dh | 1801 | tcccatctggsgccatctgtgtgtgtataagsggagsgacabaccacagagactctc | 1860 |
| Qy | 1861 | tgaagaccccgcgagaggttctctctccagctcgggsgagacctgtgaabacaccggtctc | 1920 |
| Dh | 1861 | tgaagaccccgcgagaggttctctctccagctcgggsgagacctgtgaabacaccggtctc | 1920 |
| Qy | 1921 | tgggtgccccgagaaacctgcagccccgagccccgagccccgagccccgagccccgag | 1980 |
| Dh | 1921 | tgggtgccccgagaaacctgcagccccgagccccgagccccgagccccgagccccgag | 1980 |
| Qy | 1981 | gaccctgtgcttctcatcttctgtgtgactggttcatctatccagagcatctatgacaat | 2040 |
| Dh | 1981 | gaccctgtgcttctcatcttctgtgtgactggttcatctatccagagcatctatgacaat | 2040 |
| Qy | 2041 | tattggaacttatatactctgcacaaacccacagagacaaatggtgtgagcaaaagcatctgc | 2100 |
| Dh | 2041 | tattggaacttatatactctgcacaaacccacagagacaaatggtgtgagcaaaagcatctgc | 2100 |
| Qy | 2101 | ctctacctctcgvggggtggaagactttctcatgtgaagaacgtgtgcagaagaataatgaagca | 2160 |
| Dh | 2101 | ctctacctctcgvggggtggaagactttctcatgtgaagaacgtgtgcagaagaataatgaagca | 2160 |
| Qy | 2161 | gccacaacttaaacccagctgcagaaagaaagaaataaacacacactctctgaagaattgtctgc | 2220 |
| Dh | 2161 | gccacaacttaaacccagctgcagaaagaaagaaataaacacacactctctgaagaattgtctgc | 2220 |
| Qy | 2221 | agcatctcccttaaacagagccactctctctgaagcgcctctgctctccatctgtgcgcgagag | 2280 |
| Dh | 2221 | agcatctcccttaaacagagccactctctctgaagcgcctctgctctccatctgtgcgcgagag | 2280 |
| Qy | 2281 | cccccaagccccgaatctctccaagccccctctctccatcaactcaacagcgtctgagactgtgcct | 2340 |
| Dh | 2281 | cccccaagccccgaatctctccaagccccctctctccatcaactcaacagcgtctgagactgtgcct | 2340 |
| Qy | 2341 | gctctcgtctcccgcgaaactcgtctccgtgtgactcgtgactcgtgagactcgtctccaggtc | 2400 |
| Dh | 2341 | gctctcgtctcccgcgaaactcgtctccgtgtgactcgtgactcgtgagactcgtctccaggtc | 2400 |
| Qy | 2401 | ccagaaaggaatactgtgagagaggaactagctctaacgtagaactctgagagsgagagtgcttc | 2460 |
| Dh | 2401 | ccagaaaggaatactgtgagagaggaactagctctaacgtagaactctgagagsgagagtgcttc | 2460 |
| Qy | 2461 | ctcagagaggaagaggggctctccacagctccagagagattccagagsggtgtgagagactctgacagag | 2520 |
| Dh | 2461 | ctcagagaggaagaggggctctccacagctccagagagattccagagsggtgtgagagactctgacagag | 2520 |
| Qy | 2521 | tggggagcgtctgaggtcctgagcgggtgtcctgaaagagcagagaaaggtgaaagagcagagctgaa | 2580 |
| Dh | 2521 | tggggagcgtctgaggtcctgagcgggtgtcctgaaagagcagagaaaggtgaaagagcagagctgaa | 2580 |
| Qy | 2581 | gcctgcacagaaagtctcaatgtgtgtgtctcaacggggctctgagagtttcgctgtctctctgtgagc | 2640 |
| Dh | 2581 | gcctgcacagaaagtctcaatgtgtgtgtgtctcaacggggctctgagagtttcgctgtctctctgtgagc | 2640 |
| Qy | 2641 | ctctttatcttctctcgtctgcgtctgagaggaagaagatctatcttaatgaagagatgcagtttc | 2700 |
| Dh | 2641 | ctctttatcttctctcgtctgcgtctgagaggaagaagatctatcttaatgaagagatgcagtttc | 2700 |
| Qy | 2701 | ataaagctcaagctgtctaaaatctccagaggtgtgtcactgtgttcctccagaaagcccttat | 2760 |
| Dh | 2701 | ataaagctcaagctgtctaaaatctccagaggtgtgtcactgtgttcctccagaaagcccttat | 2760 |
| Qy | 2761 | ctaaatgggaaatactgagaaagcagacatctctccaggcgtttaatctacgaaagaaagtgc | 2820 |
| Dh | 2761 | ctaaatgggaaatactgagaaagcagacatctctccaggcgtttaatctacgaaagaaagtgc | 2820 |
| Qy | 2821 | tggagctcttctctctcatgtctctctgvgcaactacacagccctgtgtgtgagactgtgctta | 2880 |
| Dh | 2821 | tggagctcttctctctcatgtctctctgvgcaactacacagccctgtgtgtgagactgtgctta | 2880 |

| | | | |
|----|------|---|------|
| QY | 2881 | tgcagaacggtcgaaaaaccccttgtaatacagaagaaatccggtttcttcttcgtcttcgccaat | 2940 |
| DB | 2881 | tgcagaacggtcgaaaaaccccttgtaatacagaagaaatccggtttcttcttcgtcttcgccaat | 2940 |
| QY | 2941 | ggttcgacgtctgcacacgttcggacagagctctccctccctcccttcggacatgctctccgct | 3000 |
| DB | 2941 | ggttcgacgtctgcacacgttcggacagagctctccctccctcccttcggacatgctctccgct | 3000 |
| QY | 3001 | ataaagaccctctgcagctcccgctgtctctctgcgaacatccctccgttgatctctctgcgaagg | 3060 |
| DB | 3001 | ataaagaccctctgcagctcccgctgtctctctgcgaacatccctccgttgatctctctgcgaagg | 3060 |
| QY | 3061 | ggatctctgcagaagggaagagagcagagcctgcagacagctgcagccacagggaggttcgaagg | 3120 |
| DB | 3061 | ggatctctgcagaagggaagagagcagagcctgcagacagctgcagccacagggaggttcgaagg | 3120 |
| QY | 3121 | ggacagggaaggcagagcaggaagctgcgttcctccatcagctctccatcgcgatccagatccagatc | 3180 |
| DB | 3121 | ggacagggaaggcagagcaggaagctgcgttcctccatcagctctccatcgcgatccagatccagatc | 3180 |
| QY | 3181 | caggaccgagagccacaaatctctccaaagaaagctccaatgaaaccaaacagccaatcttccct | 3240 |
| DB | 3181 | caggaccgagagccacaaatctctccaaagaaagctccaatgaaaccaaacagccaatcttccct | 3240 |
| QY | 3241 | tcaccaagcatabagacaatggtcattctgcataatcacaagaagatgcagagatcaatctgt | 3300 |
| DB | 3241 | tcaccaagcatabagacaatggtcattctgcataatcacaagaagatgcagagatcaatctgt | 3300 |
| QY | 3301 | ggttcgcttttcgcttcggaattccaaaacctgggcccagggcgaagtggaagaaatgcacagatattg | 3360 |
| DB | 3301 | ggttcgcttttcgcttcggaattccaaaacctgggcccagggcgaagtggaagaaatgcacagatattg | 3360 |
| QY | 3361 | ttaaacttttaaccccttaacagacacccacagccagctccaaacagtgagctctgcagacag | 3420 |
| DB | 3361 | ttaaacttttaaccccttaacagacacccacagccagctccaaacagtgagctctgcagacag | 3420 |
| QY | 3421 | agtcgacctgcagcgcagggaggaagagaagaaaagagagatgtagtctgcagcaagaag | 3480 |
| DB | 3421 | agtcgacctgcagcgcagggaggaagagaagaaaagagagatgtagtctgcagcaagaag | 3480 |
| QY | 3481 | acagatctcaattcaagggcagatgggaattgacccaggggttatagtcagtgatctccg | 3540 |
| DB | 3481 | acagatctcaattcaagggcagatgggaattgacccaggggttatagtcagtgatctccg | 3540 |
| QY | 3541 | gttccaaagagcgaaggctataattctggggggaaaaaatcagttcaagggaagtcggagga | 3600 |
| DB | 3541 | gttccaaagagcgaaggctataattctggggggaaaaaatcagttcaagggaagtcggagga | 3600 |
| QY | 3601 | ccgtgattctataatctatatcttctcccttcaaacgctgagtgaaattctgcagatcaag | 3660 |
| DB | 3601 | ccgtgattctataatctatatcttctcccttcaaacgctgagtgaaattctgcagatcaag | 3660 |
| QY | 3661 | gtagtaactgcagcctgtaagaattactagttcttcctcttaagaaactcttctctcgt | 3720 |
| DB | 3661 | gtagtaactgcagcctgtaagaattactagttcttcctcttaagaaactcttctctcgt | 3720 |
| QY | 3721 | ggaggttcagcagcaaaagggcatacccggttctctttaaagcggagaagaaacatctccaaag | 3780 |
| DB | 3721 | ggaggttcagcagcaaaagggcatacccggttctctttaaagcggagaagaaacatctccaaag | 3780 |
| QY | 3781 | taaaagccaaacagatctcaagcctcaggtcctgcagcatatagatctgtgttttgcgaat | 3840 |
| DB | 3781 | taaaagccaaacagatctcaagcctcaggtcctgcagcatatagatctgtgtgttttgcgaat | 3840 |
| QY | 3841 | catctcagcgaatgttatactctgcgatccagaataatgagactagtaaccttcgttcagctg | 3900 |
| DB | 3841 | catctcagcgaatgttatactctgcgatccagaataatgagactagtaaccttcgttcagctg | 3900 |
| QY | 3901 | taaaataaacaccacgctgtgtaaatggtctcaagttccaggtctaaactgcagaaacaaatcaaaa | 3960 |
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RESULT 2
V51361
ID V51361 standard; DNA; 5299 BP.
XX
AC V51361;
XX
DT 27-OCT-1998 (first entry)
XX
DE Human TIGR promoter region DNA.
XX
KW TIGR: trabecular meshwork induced glucocorticoid response protein; human;
   diagnosis: glaucoma; polymorphism; steroid sensitivity; ss.
XX
OS Homo sapiens.
XX
PN W09832850-A1.
XX
PD 30-JUL-1998.
XX
PE 09-JAN-1998; 98MO-US00468.
XX
PR 26-SEP-1997; 97US-0938669.
XX
PR 28-JAN-1997; 97US-0791154.
XX
PA (REGC ) UNIV CALIFORNIA.
XX
PI Chen H, Chen P, Nguyen TD, Polansky JR;
XX
DR WPI; 1998-427946/36.
XX
PT Use of TIGR nucleic acid sequences - used for, e.g. developing
   products for diagnosis, prognosis and treatment of glaucoma
XX
PS Claim 34; Fig 1; 105bp; English.
XX
CC This sequence is a trabecular meshwork induced glucocorticoid response
   protein (TIGR) promoter region which is used in a method for diagnosing
   CC glaucoma in a patient. The method involves the detection of polymorphisms
   CC whose presence is predictive of a mutation affecting TIGR response in the
   CC patient and can be diagnostic of glaucoma or steroid sensitivity. Base
   CC substitutions and base additions upstream of and within TIGR exons can
   CC also be used to diagnose glaucoma.
XX
SQ Sequence 5299 BP; 1482 A; 1151 C; 1235 G; 1431 T; 0 other;

Query Match 99.5%; Score 5246.4; DB 19; Length 5299;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 5269; Conservative 0; Mismatches 1; Indels 2; Gaps 2;

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Oy 4260 ttgtttttaacacacttcaacaaatataacattatctcctctgagaaatgagacataa 4319
Db 4260 ttgtttttaacacacttcaacaaatataacattatctcctctgagaaatgagacataa 4319
Oy 4320 actcaagtggaataaagagtaacccgtgatatgtgtcatttaacaaatagaaatcagagact 4379
Db 4320 actcaagtggaataaagagtaacccgtgatatgtgtcatttaacaaatagaaatcagagact 4379
Oy 4380 ttataacataatataagtggtgcagataagtgtaagtgaaatattatactcaaaact 4439
Db 4380 ttataacataatataagtggtgcagataagtgtaagtgaaatattatactcaaaact 4439
Oy 4440 acttgaaattagaccctcctcgtgagacttggttttaacataataaacaagtttaa 4499
Db 4440 acttgaaattagaccctcctcgtgagacttggttttaacataataaacaagtttaa 4499

| | | | |
|----------|-------------|---|------|
| Oy | 4500 | aatttgtaattttgataaactaatctaatcttaacatttggttttccttctgttaactatact | 4559 |
| Db | 4500 | aattttgtaatttttgcataaactaatcttaacttaacttaactttgttttccttgcataactatact | 4559 |
| Oy | 4560 | tataataattgaaaaaacactctctctctgagaagaagttcccccagaatttcacacatgagaattcttg | 4619 |
| Db | 4560 | tataataattgaaaaaacactctctctctgagaagaagttcccccagaatttcacacatgagaattcttg | 4619 |
| Oy | 4620 | gcaatgcacacacacacagagtaagaactgtaattagaggctaaacattgacattggtgtgcctgag | 4679 |
| Db | 4620 | gcatgcacacacacacagagtaagaactgtaattagaggctaaacattgacattggtgtgcctgag | 4679 |
| Oy | 4680 | atgcagaagaactgaaattatgaagaagttctccccaagaatacacagattggtttttaagccaagggtc | 4739 |
| Db | 4680 | atgcagaagaactgaaattatgaagaagttctccccaagaatacacagattggtttttaagccaagggtc | 4739 |
| Oy | 4740 | gagggggggaatactgcgcgtctctataagaatgtctctccctggaagcctgtgtaggggtgtctc | 4799 |
| Db | 4740 | gagggggggaatactgcgcgtctctataagaatgtctctccctggaagcctgtgtaggggtgtctc | 4799 |
| Oy | 4800 | cctctgtctctgtgcgcgcgtcttaattttctctctgtccctgttaagctcttaagaagaactgtct | 4859 |
| Db | 4800 | cctctgtctctgtgcgcgcgtcttaattttctctctgtccctgttaagctcttaagaagaactgtct | 4859 |
| Oy | 4860 | tggatctccaggtctccagcatagtgctctggaacagtgacaggtctctcaatgattgagtttcgaga | 4919 |
| Db | 4860 | tggatctccaggtctccagcatagtgctctggaacagtgacaggtctctcaatgattgagtttcgaga | 4919 |
| Oy | 4920 | gtgaattggaataataaactagaataataatctctgttgaatactgacacacagtagtctctg | 4979 |
| Db | 4920 | gtgaattggaataataaactagaataataatctctgttgaatactgacacacagtagtctctg | 4979 |
| Oy | 4980 | ggtgtgaagtgtgtgtgaagt | 5039 |
| Db | 4980 | ggtgtgaagtgtgtgtgaagt | 5039 |
| Oy | 5040 | atagagaacattatcttgaggctatgtgtgcataaaatttggaatgctctcttttaaaaaagaact | 5099 |
| Db | 5040 | atagagaacattatcttgaggctatgtgtgcataaaatttggaatgctctcttttaaaaaagaact | 5099 |
| Oy | 5100 | ccaaacagaactctctggaaggttaattttcttaagaactctgtctgtgacagcgtggaagcaaaccc | 5159 |
| Db | 5100 | ccaaacagaactctctggaaggttaattttcttaagaactctgtctgtgacagcgtggaagcaaaccc | 5159 |
| Oy | 5160 | ccctgtgcacagcccccacacagcctcaagtggtgcacactctgtcttcccccatgagaaggtc | 5219 |
| Db | 5160 | ccctgtgcacagcccccacacagcctcaagtggtgcacactctgtcttcccccatgagaaggtc | 5219 |
| Oy | 5220 | ggctcccccagtatataataaacctctctggaagcctcggaagcagtagacagcaagaag | 5271 |
| Db | 5220 | ggctcccccagtatataataaacctctctggaagcctcggaagcagtagacagcaagaag | 5271 |
| RESULT 3 | | | |
| ID | V51362 | standard; DNA; 5300 BP. | |
| XX | V51362: | | |
| AC | 27-OCT-1998 | (first entry) | |
| DT | xx | | |
| XX | xx | | |
| DE | xx | Human TIGR promoter mutant TIGRmt1 DNA. | |
| KW | xx | TIGR: trabecular meshwork induced glucocorticoid response protein; human; | |
| KW | xx | diagnosis: gliucoma; polymorphism; steroid sensitivity; mutant; ss. | |
| OS | xx | Homo sapiens. | |
| OS | xx | Synthetic. | |
| PH | Key | Location/Qualifiers | |
| PH | 4337 | | |
| TT | mutation | /tag= a | |

FT /note= "Wild type C is replaced by G"
XX
XX
PN W09832850-A1.
XX
XX 30-JUL-1998.
XX
XX
XX 09-JAN-1998; 98WO-US00468.
XX
XX 26-SEP-1997; 97US-0938659.
XX 28-JAN-1997; 97US-0791134.
XX
XX (REGC) UNIV CALIFORNIA.
XX
XX
XX Chen H, Chen P, Nguyen TD, Polansky JR;
XX
XX WPI: 1998-427946/36.
XX
XX
XX Use of TIGR nucleic acid sequences - used for, e.g. developing
XX products for diagnosis, prognosis and treatment of glaucoma
XX
XX
XX Disclosure: Fig 2; 105pp; English.
XX
XX
XX This sequence is a trabecular meshwork induced glucocorticoid response
XX protein (TIGR) promoter mutant, TIGRmt1, which is used in a method for
XX diagnosing glaucoma in a patient. The method involves the detection of
XX polymorphisms whose presence is predictive of a mutation affecting TIGR
XX response in the patient and can be diagnostic of glaucoma or steroid
XX sensitivity. Base substitutions and base additions upstream of and within
XX TIGR exons can also be used to diagnose glaucoma.
XX
XX Sequence 5300 BP; 1482 A; 1151 C; 1236 G; 1431 T; 0 other;
XX

[illegible]

| | | | |
|----|------|---|------|
| Oy | 541 | ggtctacctcttggggagagcagatcttcggagaagtcatgttgcgaagaagacataacataac | 600 |
| Db | 541 | ggcaccctctcttggggagagcagatcttcggagaagtcatgttgcgaagaagacataacataac | 600 |
| Oy | 601 | agcaaaatcgaataatccgcgaatctgcagggaggaataatgggagatctgggaagctttcatac | 660 |
| Db | 601 | agcaaaatcgaataatccgcgaatctgcagggaggaataatgggagatctgggaagctttcatac | 660 |
| Oy | 661 | agtgatattaggaattgacacattgtctgcacaacacctcccgctctataccaggggaacaaa | 720 |
| Db | 661 | agtgatttaggcagttgcacattgtctgcacaacacctcccgctctataccaggggaacaaa | 720 |
| Oy | 721 | attgacccgggtcgaagccttgacattccaagggaaatatgaaaaactcgagacaaacaaa | 780 |
| Db | 721 | attgacccgggtcgaagccttgacattccaagggaaatatgaaaaactcgagacaaacaaa | 780 |
| Oy | 781 | gacatgtgttaaaaggcacaacagacaatttgagcccttcagaagcagatgccccctacga | 840 |
| Db | 781 | gacatgtgttaaaaggcacaacagacaatttgagcccttcagaagcagatgccccctacga | 840 |
| Oy | 841 | ggagcccttgagcattctgccttcaggaagaagccagttcttcgaaggagacttaagaatac | 900 |
| Db | 841 | ggagcccttgagcattctgccttcaggaagaagccagttcttcgaaggagacttaagaatac | 900 |
| Oy | 901 | ttggaagaatcatgaatttttaacacattttaagtataaacaatatgcatgtcataatag | 960 |
| Db | 901 | ttggaagaatcatgaatttttaacacattttaagtataaacaatatgcatgtcataatag | 960 |
| Oy | 961 | tttgaacatgtgtcccaattttaaaagtcagacataagaataaactgtgtcccgctcc | 1020 |
| Db | 961 | tttgaacatgtgtcccaattttaaaagtcagacataagaataaactgtgtcccgctcc | 1020 |
| Oy | 1021 | ggaataggatcagaataatcatatgaataatcactgtgtcccaatcctaaattttcagaatgac | 1080 |
| Db | 1021 | ggaataggatcagaataatcatatgaataatcactgtgtcccaatcctaaattttcagaatgac | 1080 |
| Oy | 1081 | tgctaatgcccccaacacagagcccgatgtgtctgacatacaaacacatcatacccaa | 1140 |
| Db | 1081 | tgctaatgcccccaacacagagcccgatgtgtctgacatacaaacacatcatacccaa | 1140 |
| Oy | 1141 | gtgcctcaacacattgtttaaagtgctatccagtagagttcccatattaaatgtccacctccc | 1200 |
| Db | 1141 | gtgcctcaacacattgtttaaagtgctatccagtagagttcccatattaaatgtccacctccc | 1200 |
| Oy | 1201 | tgctgacagcccatcccgctcccaacagagatctcccaactagatcttcgatcaagatgt | 1260 |
| Db | 1201 | tgctgacagcccatcccgctcccaacagagatctcccaactagatcttcgatcaagatgt | 1260 |
| Oy | 1261 | tacagccagaagaactcgttgaggggtgaggggtcgtgtcttaacactaactgtatgctaac | 1320 |
| Db | 1261 | tacagccagaagaactcgttgaggggtgaggggtcgtgtcttaacactaactgtatgctaac | 1320 |
| Oy | 1321 | accctgagcctaacctgcgaacacctctgcctcccaaggtttcaagaatattcccgctccaacctcc | 1380 |
| Db | 1321 | accctgagcctaacctgcgaacacctctgcctcccaaggtttcaagaatattcccgctccaacctcc | 1380 |
| Oy | 1381 | cgcgtaagctggagactacaagcgcagacgcccggcgaatttttgatgtttagttagagatggg | 1440 |
| Db | 1381 | cgcgtaagctggagactacaagcgcagacgcccggcgaatttttgatgtttagttagagatggg | 1440 |
| Oy | 1441 | gtttcacacataatagcccggtctgtctctgaactcctgacactctagatgtgatacccaacttc | 1500 |
| Db | 1441 | gtttcacacataatagcccggtctgtctctgaactcctgacactctagatgtgatacccaacttc | 1500 |
| Oy | 1501 | agcctcttaagaagtgctggggttatacagatctgataccggtccggccgaagggttaagt | 1560 |
| Db | 1501 | agcctcttaagaagtgctggggttatacagatctgataccggtccggccgaagggttaagt | 1560 |
| Oy | 1561 | tttaataagggaataactgtgaattgttttaacaaaccaaaggggaataacgaacaaagctgtga | 1620 |
| Db | 1561 | tttaataagggaataactgtgaattgttttaacaaaccaaaggggaataacgaacaaagctgtga | 1620 |
| Oy | 1621 | taattttcaagggaattcttggaattgggaataatgtgtcattgagctggcctctgactagctccacac | 1680 |

| | | | |
|----|------|---|------|
| Db | 1621 | taattcacaaggagatcttcctgaggacatgaggaaatgagccacagagctgcgcccaagctcccaagac | 1680 |
| Qy | 1681 | caactggtccatccacaacattctctctccctccatctccatcttccagagctaaagttaaactttatct | 1740 |
| Db | 1681 | caactggtccatccatcaactcttctctccctccatctccatcttccagagctaaagttaaactttatct | 1740 |
| Qy | 1741 | caaccaagctcttgtagtaagctccacatctgtaactgaataaagatatacataaactag | 1800 |
| Db | 1741 | caccacagctcttttgtagtaagctccacatctgtaactgaataaagatatacataaactag | 1800 |
| Qy | 1801 | ttccatttgggggcacatcttgtagttagtaaggaggagagagagcaatacccaagagactccct | 1860 |
| Db | 1801 | ttccacatttgggggcacacatctgtagttagtaaggaggagagagagagcaatacccaagagactccct | 1860 |
| Qy | 1861 | tgaagccccccggcagagaggtttctctctccacagcttgaggggagcccccttgcaagcaccgggggtcc | 1920 |
| Db | 1861 | tgaagagccccccggcagagaggtttctctctccacagcttgaggggagcccccttgcaagcaccgggggtcc | 1920 |
| Qy | 1921 | tgggtgtctctgagcaaacctgtcacagccgtgtgcacatgtagttgtttagttaatactctctag | 1980 |
| Db | 1921 | tgggtgtgtctctgagcaaacctgtcacagccgtgtgcacatgtagttgtttagttaatactctctag | 1980 |
| Qy | 1981 | gaccctgtgtctctctatctctctgtgtgagatctgttcaatacccaagagattcaatgtgaacatt | 2040 |
| Db | 1981 | gaccctgtgtgtctctctatctctctgtgtgagatctgttcaatacccaagagattcaatgtgaacatt | 2040 |
| Qy | 2041 | tattgtatctatctatctatctgtccagagacacacagagacaaaatgtgtgagcacaagctacatctg | 2100 |
| Db | 2041 | tattgtatgtactatctatctgtccagagacacacagagacaaaatgtgtgagcacaagctacatctg | 2100 |
| Qy | 2101 | ctctacctctgttgtagaggtgacagattctctcatgtagaagaagctgtcagagaagaataataagcca | 2160 |
| Db | 2101 | ctctacctctctgttgtagaggtgacagattctctcatgtagaagaagctgtcagagaagaataataagcca | 2160 |
| Qy | 2161 | gcccaactttaaaccacatgtgtgaagaagaaggagaaataaacaacatttgaagaataatgtgcgc | 2220 |
| Db | 2161 | gcccaactcttaaacccaatgtgtcgaagaagaaggagaaataaacaacattctgaagaataatgtgcgc | 2220 |
| Qy | 2221 | agcatccctctaaacaaaggccacactctccctctgagcccccctgtctctccatctgtgcgcggagag | 2280 |
| Db | 2221 | agcatccctcttaaacaaaggccacactctccctctgagcccccctgtctctccatctgtgcgcggagag | 2280 |
| Qy | 2281 | cccccaagcccgagctctctccaaagcctctctctccatctcaatgatacagcgctgtcagcgct | 2340 |
| Db | 2281 | cccccaagcccgagctctctccaaagcctctctctccatctcaatgatacagcgctgtcagcgct | 2340 |
| Qy | 2341 | gctctcggtctccggtagaatactcctgtgtgcatctgtagcctgaggagatcccttggctcccaaggtc | 2400 |
| Db | 2341 | gctctcggtctctccggtagaatactcctgtgtgcatctgtagcctgaggagatcccttggctcccaaggtc | 2400 |
| Qy | 2401 | ccgaagaaggaatactgtagagagagaaactagctcaaacgagagaactctgagaggagacagtgttcc | 2460 |
| Db | 2401 | ccgaagaaggaatactgtagagagagagaaactagctcaaacgagagaactctgagaggagacagtgttcc | 2460 |
| Qy | 2461 | ctcagagaggaagaagggcctccacgctccagagaaattcccaagagatgtgggagctctcagaggag | 2520 |
| Db | 2461 | ctcagagaggaagaagggcctccacgctccagagaaattcccaagagatgtgggagctctcagaggag | 2520 |
| Qy | 2521 | tggggagacgctcgagggtcgtcgaacagggtgtctgaaaaaggccaggaagaagtgaaaaaggccaaaggtctgaa | 2580 |
| Db | 2521 | tggggagacgctcgagggtcgtcgaacagggtgtctgaaaaaggccaggaagaagtgaaaaaggccaaaggtctgaa | 2580 |
| Qy | 2581 | gctgtcccaagatgtctacgtctgttcaacgggagctggagaaattcttcggtctgtctctctgtgaagc | 2640 |
| Db | 2581 | gctgtcccaagatgtctacgtctgttcaacgggagctggagaaattcttcggtctgtctctctgtgtgaagc | 2640 |
| Qy | 2641 | ctttcttctctctctctctgtcttgtagaggaagaagaatctatattcatgaaaggatgtcagtttc | 2700 |
| Db | 2641 | ctttttatctctctctctctgtcttgtagaggaagaagaatctatattcatgaaaggatgtcagtttc | 2700 |
| Qy | 2701 | ataaagctcagctgtttaaaatctccaaagggtgtgcacatggtttctctctcaggaagcctttat | 2760 |

Db 2701 ataaagtcagctgttaaaattccaaggtgtgtcaatgggttttcttcacgaagcccttat 2760
QY ttaaigtggaataaagaagcagagctcatattccaaaggccgttaattcaacgaagaagagac 2820
QY 2761 ttaaivggaaataaagaagagagctcaattccaaaggccgttaattccgaagaagagac 2820
Db 2821 tgaagctcttcttcatagtctctctggtgcaactacatcaagccctgtgtgagacttgctta 2880
Db 2821 tgaagctcttcttcatagtctctctggtgcaactacatcaagccctgtgtgagacttgctta 2880
QY 2881 tgaagaacggttcgaaaaaccttgaatacagaagacacggttctctctcgtgtccatc 2940
Db 2881 tgaagaacggttcgaaaaaccttgaatacagaagacacggttctctctcgtgtccatc 2940
QY 2941 ggttgcctgttgcgaacccgttgagcaaggtctctctctcccggtgacatagctctcgtc 3000
Db 2941 ggttgcctgttgcgaacccgttgagcaaggtctctctctcccggtgacatagctctcgtc 3000
QY 3001 ataaagacccttcgaacccctcgtgtctctgtaaacacttccctgtgattctctgtgaaggg 3060
Db 3001 ataaagacccttcgaacccctcgtgtctctgtaaacacttccctgtgattctctgtgaaggg 3060
QY 3061 ggaatgttgaagagggaagaagagcagagctggaacagctgaagccaagggaggtgaaggg 3120
Db 3061 ggaatgttgaagagggaagaagagcagagctggaacagctgaagccaagggaggtgaaggg 3120
QY 3121 ggaacaaagagcagcagaagagctgggtgtccatcagttctctcatgatacagctcagactc 3180
Db 3121 ggaacaaagagcagcagaagagctgggtgtccatcagttctctcatgatacagctcagactc 3180
QY 3181 caaggaacgagagcacaatctctcagaagaagctcaatgaacccaacagccacactttccct 3240
Db 3181 caaggaacgagagcacaatctctcagaagaagctcaatgaacccaacagccacactttccct 3240
QY 3241 tcccttaagcatalgaaacaaatgttcgtccaaataaccaaagaatgcagagactaaactggt 3300
Db 3241 tcccttaagcatalgaaacaaatgttcgtccaaataaccaaagaatgcagagactaaactggt 3300
QY 3301 ggaagcttttgccttcgcatctcaaaaacttggcagagcagaagtggaaaatgccagaagttg 3360
Db 3301 ggaagcttttgccttcgcatctcaaaaacttggcagagcagaagtggaaaatgccagaagttg 3360
QY 3361 ttaaacttttcaacccctgaacagcaccacagcagctcagagactgactgtcgaacagcag 3420
Db 3361 ttaaacttttcaacccctgaacagcaccacagcagctcagagactgactgtcgaacagcag 3420
QY 3421 agtgaacctgcagcgcagggggaagaagaagaagaagaggtatgctatgaagcaagaag 3480
Db 3421 agtgaacctgcagcgcagggggaagaagaagaagaagaggtatgctatgaagcaagaag 3480
QY 3481 acagatctcatcaaaagggcaggtggaaattgacacagggatatagtccacagtatcccttg 3540
Db 3481 acagatctcatcaaaagggcaggtggaaattgacacagggatatagtccacagtatcccttg 3540
QY 3541 gttctcaggaagcagggctataatgttggggggaaaaaatcagttccaagggaggtccggaga 3600
Db 3541 gttctcaggaagcagggctataatgttggggggaaaaaatcagttccaagggaggtccggaga 3600
QY 3601 ccttgatcttaatactataatttctcctcttaacagcttgagtaattcttgaagaatccaag 3660
Db 3601 ccttgatcttaatactataatttctcctcttaacagcttgagtaattcttgaagaatccaag 3660
QY 3661 gttgttaactgaagctgttaaaatactactagtctctccttataggaactcttctctgtc 3720
Db 3661 gttgttaactgaagctgttaaaatactactagtctctccttataggaactcttctctgtc 3720
QY 3721 ggaatctcagcagcagaaggaatcccgcttctctttaaaggaagaagaacatcccttaagag 3780
Db 3721 ggaatctcagcagcagaaggaatcccgcttctctttaaaggaagaagaacatcccttaagag 3780
QY 3781 taaagccaaacagattcaagccttagtctctgtcgtacataatgattgtgtttttgaaaaat 3840
Db 3781 taaagccaaacagattcaagccttagtctctgtcgtacataatgattgtgtttttgaaaaat 3840

QY 3841 catttcagcagatgttactatctgattccagaataatagacaaatcaccccttgcgtcag 3900
Db 3841 catttcagcagatgttactatctgattccagaataatagacaaatcaccccttgcgtcag 3900
QY 3901 taaacaacaacccagttgtaaatgtctcaagtctcaagcttaactgcagaaaccaataca- 3959
Db 3901 taaacaacaacccagttgtaaatgtctcaagtctcaagcttaactgcagaaaccaataca- 3959
QY 3960 aagaaataagaattcttagagcaaaactgttttcccaacatctggaaggtgtgtccgaagg 4019
Db 3961 aagaaataagaattcttagagcaaaactgttttcccaacatctggaaggtgtgtccgaagg 4019
QY 4020 cagtttggaataattactacacagtatgacacagctgtgtgtgtgtatcaacaacataag 4079
Db 4020 cagtttggaataattactacacagtatgacacagctgtgtgtgtgtatcaacaacataag 4079
QY 4080 ttgctcaaaagcgaatcatatttcaagtgtgttaaaagttaactctgacagtttggtaata 4139
Db 4080 ttgctcaaaagcgaatcatatttcaagtgtgttaaaagttaactctgacagtttggtaata 4139
QY 4140 ttatattgctaatgtccattgtccttcttctctctgtgggttcaataatgttaagca 4199
Db 4140 ttatattgctaatgtccattgtccttcttctctctgtgggttcaataatgttaagca 4199
QY 4200 ggaattatcaactacagttccagaagccgtgtgaatttgaatgaggaagaataatatacat 4259
Db 4200 ggaattatcaactacagttccagaagccgtgtgaatttgaatgaggaagaataatatacat 4259
QY 4260 ttgttttcaacaccccttcaactaaatttaacatttatttccattgtggaataagccataa 4319
Db 4260 ttgttttcaacaccccttcaactaaatttcaactttatttccattgtggaataagccataa 4319
QY 4320 acccaaggtgtataacagtaacctgtgtatttgttcaataccaatgaaatccagaacat 4379
Db 4320 acccaaggtgtataacagtaacctgtgtatttgttcaataccaatgaaatccagaacat 4379
QY 4380 tttaatactaatatcaagttgttcagatacgttgaatgtaaatatttataccaaact 4439
Db 4380 tttaatactaatatcaagttgttcagatacgttgaatgtaaatatttataccaaact 4439
QY 4440 actttgaataatgaacctcctcgtgtgattctgttttaacataataataaactgtttaa 4499
Db 4440 actttgaataatgaacctcctcgtgtgattctgttttaacataataataaactgtttaa 4499
QY 4500 aatttgaataatttgaataatcatattcatattcatatttcttctctgttaataattc 4559
Db 4500 aatttgaataatttgaataatcatattcatattcatatttcttctctgttaataattc 4559
QY 4560 tatataattgaaacaatctcttcggaagaaggtccccaagattccacaagaagagttcttg 4619
Db 4560 tatataattgaaacaatctcttcggaagaaggtccccaagattccacaagaagagttcttg 4619
QY 4620 gcatctcacacacacagtaagaagcagatttaagaagctaaacatctgacatgtggcctgag 4679
Db 4620 gcatctcacacacacagtaagaagcagatttaagaagctaaacatctgacatgtggcctgag 4679
QY 4680 atgcaagactgaaactagaagaattcttcccaagaatacaacagttgttttaagctaaaggt 4739
Db 4680 atgcaagactgaaactagaagaattcttcccaagaatacaacagttgttttaagctaaaggt 4739
QY 4740 gaaggggggaatactgtccgcttctataaggaatgtctcccggtggagccctgtgaaggtgtc 4799
Db 4740 gaaggggggaatactgtccgcttctataaggaatgtctcccggtggagccctgtgaaggtgtc 4799
QY 4800 ccttctgtctcgtgctgttataatttctctctgttccctgtcaagctcttaaggaactgtt 4859
Db 4800 ccttctgtctcgtgctgttataatttctctctgttccctgtcaagctcttaaggaactgtt 4859
QY 4860 tgaatctcgaagttcccaagcataatgtcccgcaaggtcctcaatgaagtcttcagaa 4919
Db 4860 tgaatctcgaagttcccaagcataatgtcccgcaaggtcctcaatgaagtcttcagaa 4919

[illegible]

| | | |
|--------|---|---|
| RESULT | 4 | |
| ID | V51363 | |
| XX | V51363 standard; DNA; 5300 BP. | |
| XX | | |
| AC | V51363; | |
| XX | | |
| DT | 27-OCT-1998 (first entry) | |
| XX | | |
| DE | Human TIGR promoter mutant TIGRmt2 DNA. | |
| XX | | |
| KW | TIGR; trabecular meshwork induced glucocorticoid response protein; human; | |
| RW | diagnosis; glaucoma; polymorphism; steroid sensitivity; mutant; ss. | |
| XX | | |
| OS | Homo sapiens. | |
| OS | Synthetic. | |
| XX | | |
| FH | Key | Location/Qualifiers |
| FT | mutation | 4950 |
| FT | | /*tag- a |
| FT | | /note- "Wild-type C is replaced with T" |
| XX | | |
| PN | W09832850-A1. | |
| XX | | |
| PD | 30-JUL-1998. | |
| XX | | |
| PF | 09-JAN-1998; 98NO-US00468. | |
| XX | | |
| PR | 26-SEP-1997; 97US-0938669. | |
| PR | 28-JAN-1997; 97US-0791154. | |
| XX | | |
| PA | (REGC) UNIV CALIFORNIA. | |
| XX | | |
| PI | Chen H, Chen P, Nguyen TD, Polansky JR; | |
| XX | | |
| DR | WPI: 1998-427946/36. | |
| PT | | |
| PT | Use of TIGR nucleic acid sequences - used for, e.g. developing | |
| XX | products for diagnosis, prognosis and treatment of glaucoma | |
| XX | | |
| PS | Disclosure: Fig 2; 105pp; English. | |
| XX | | |
| CC | This sequence is a trabecular meshwork induced glucocorticoid response | |
| CC | protein (TIGR) promoter mutant, TIGRmt2, which is used in a method for | |
| CC | diagnosing glaucoma in a patient. The method involves the detection of | |
| CC | polymorphisms whose presence is predictive of a mutation affecting TIGR | |
| CC | response in the patient and can be diagnostic of glaucoma or steroid | |
| CC | sensitivity. Base substitutions and base additions upstream of and within | |
| CC | TIGR exons can also be used to diagnose glaucoma. | |

XX Sequence 5300 BP; 1482 A; 1151 C; 1235 G; 1432 T; 0 other
SQ

| | | | | |
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| Query Match | 99.58; | Score 5244.8; | DB 19; | Length 5300; |
| Best Local Similarity | 99.98; | Pred. NO. 0; | | |
| Matches 5268; | Conservative | 0; | Mismatches 2; | Indels 2; |
| | | | Gaps | 2; |

[illegible]

| | | | |
|----|------|--|------|
| Dp | 691 | ctttagacaatgggcccccaattctataaaggacagacatacagataaaacgtgccagctcc | 1020 |
| Oy | 1021 | ggaataggctcagaaatcatagaaatcaactgtgtcccatctcnaactttctagaatgac | 1080 |
| Dp | 1021 | ggaataggctcagaaatcatagaaatcaactgtgtcccatctcnaactttctagaatgac | 1080 |
| Oy | 1081 | tgatataggccctcacacacacagagccgagtggtgtctgacctacaaacacatactacaaccaa | 1140 |
| Dp | 1081 | tgatataggccctcacacacacagagccgagtggtgtctgacctacaaacacatactacaaccaa | 1140 |
| Oy | 1141 | gtgtccttaaaccatgtgttaaaagtgtcatctccaaataggtcccatatgaatgtccactcccc | 1200 |
| Dp | 1141 | gtgtccttaaaccatgtgttaaaagtgtcatctccaaataggtcccatatgaatgtccactcccc | 1200 |
| Oy | 1201 | tgtgtacagcccatcccgctccacacagagagctcccccctctagaaactctgtacatacagatgt | 1260 |
| Dp | 1201 | tgtgtacagcccatcccgctccacacagagagctcccccctctagaaactctgtacatacagatgt | 1260 |
| Oy | 1261 | tacacagccagaagctccggtgaaagggtgaagggtctgtgtctatacaccataccgtatgtctac | 1320 |
| Dp | 1261 | tacacagccagaagctccggtgaaagggtgaagggtctgtgtctatacaccataccgtatgtctac | 1320 |
| Oy | 1321 | accctgaatctcaactgtgcaaacctctgtccctcccaaggtttcaaggaattctccctgtctagctcc | 1380 |
| Dp | 1321 | accctgaatctcaactgtgcaaacctctgtccctcccaaggtttcaaggaattctccctgtctagctcc | 1380 |
| Oy | 1381 | cggcgtaagcttgagacatacagacagacagcccgccgacaaatttttgatgtttagtagagaatggg | 1440 |
| Dp | 1381 | cggcgtaagcttgagacatacagacagacagcccgccgacaaatttttgatgtttagtagagaatggg | 1440 |
| Oy | 1441 | gtttccacacatactaaagcccggtctgtgtcttgaaactctgtaaccttcagatgtgaatccacacactc | 1500 |
| Dp | 1441 | gtttccacacatactaaagcccggtctgtgtcttgaaactctgtaaccttcagatgtgaatccacacactc | 1500 |
| Oy | 1501 | agcctccttaaaagtgtcgtggaattacagagcatgaagtcaacggcgccgagcaaggttcagatgtc | 1560 |
| Dp | 1501 | agcctccttaaaagtgtcgtggaattacagagcatgaagtcaacggcgccgagcaaggttcagatgtc | 1560 |
| Oy | 1561 | ttaaataagagaaataactgtgaaatgtgtttacttaaaaccaaagagagaaagacaaagaactgtga | 1620 |
| Dp | 1561 | ttaaataagagaaataactgtgaaatgtgtttacttaaaaccaaagagagaaagacaaagaactgtga | 1620 |
| Oy | 1621 | ttaattcaaggaattctctgagaaatgaggaatctgtgacatgaagctgtccctgtctagttccagac | 1680 |
| Dp | 1621 | ttaattcaaggaattctctgagaaatgaggaatctgtgacatgaagctgtccctgtctagttccagac | 1680 |
| Oy | 1681 | caactgtgtcctatcaactttctctccctcaactcattttcaaggtcaagtattacatttattc | 1740 |
| Dp | 1681 | caactgtgtcctatcaactttctctccctcaactcattttcaaggtcaagtattacatttattc | 1740 |
| Oy | 1741 | caacaaatgtctttgtggtgaagaagcccccacacacgtgttaaccgaaataaaggataatacaataactag | 1800 |
| Dp | 1741 | caacaaatgtctttgtggtgaagaagcccccacacacgtgtgttaaccgaaataaaggataatacaataactag | 1800 |
| Oy | 1801 | tcccaattctggggccaactcgtgtgtgtgtataagagagagagagagacataccccagaaactcct | 1860 |
| Dp | 1801 | tcccaattctggggccaactcgtgtgtgtgtgtataagagagagagagagacataccccagaaactcct | 1860 |
| Oy | 1861 | tgaagagcccccggcagagaggttctctctccagctgtggggagagccctgcagacacccggggtcc | 1920 |
| Dp | 1861 | tgaagagcccccggcagagaggttctctctccagctgtggggagagccctgcagacacccggggtcc | 1920 |
| Oy | 1921 | tgggtgtgtccctgagagaaacctgtgcacagcccggtgcacatgtgtttgtttataactctcagg | 1980 |
| Dp | 1921 | tgggtgtgtccctgagagaaacctgtgcacagcccggtgcacatgtgtttgtttataactctcagg | 1980 |
| Oy | 1981 | gaactgtgtacttctatctctgtgtgtacatcgtttcatctacatccagagcatctatgacaatt | 2040 |
| Dp | 1981 | gaactgtgtacttctatctctgtgtgtacatcgtttcatctacatccagagcatctatgacaatt | 2040 |
| Oy | 2041 | tattgtatcttatatcatctgcacagacacagagacaaatgtgtgaacaaagcagtaactgtc | 2100 |

| | | | |
|----|------|--|------|
| Dh | 2041 | tatvgaagtaactatatactcgcagacacccagagacaaaaatgvtgagccaaagcagtcactgc | 2100 |
| Qy | 2101 | ccctactctgtctgagagvtgacagttcttcaatgaaagcgtccagaaagaaaataaagca | 2160 |
| Dh | 2101 | ccctactctctgagagagvtgacagttcttcaatgaaagcgtccagaaagaaaataaagca | 2160 |
| Qy | 2161 | gccaaactaaaaacccagvtctgtaaaagaaagaaataaaacacactctgtaaagaaatgtgcgc | 2220 |
| Dh | 2161 | gccaaactaaaaacccagvtctgtaaaagaaagaaataaaacacacactctgtaaagaaatgtgcgc | 2220 |
| Qy | 2221 | agcattccctttaaacaagagccactctccctagcgcgccctctgctcccaactgtgccccgaag | 2280 |
| Dh | 2221 | agcattccctttaaacaagagccactctccctagcgcgccctctgctcccaactgtgccccgaag | 2280 |
| Qy | 2281 | cccccaagccccagatctctcccaagccctctctccatcaatgtaacagcgtccagcttgccct | 2340 |
| Dh | 2281 | cccccaagccccagatctctcccaagccctctctctccatcaatgtaacagcgtccagcttgccct | 2340 |
| Qy | 2341 | gacctgcttcccgvtgaatctgctctctgtgtgcatctctgagcttgagagctcttgccccaggtc | 2400 |
| Dh | 2341 | gacctgcttcccgvtgaatctgctctctgtgtgtgcatctctgagcttgagagctcttgccccaggtc | 2400 |
| Qy | 2401 | ccaaagaaagaaatctgagagagagaaactagctcaagagagaaatctgagagagaaatgtgttc | 2460 |
| Dh | 2401 | ccaaagaaagaaatctgagagagagaaactagctcaagagagaaatctgagagagaaatgtgttc | 2460 |
| Qy | 2461 | ctcaaaagagaaagagagccctccacagctccagagaaatctccagagaggttgagagactcgagagag | 2520 |
| Dh | 2461 | ctcaagagagaaagagagccctccacagctccagagaaatctccagagaggttgagagactcgagagag | 2520 |
| Qy | 2521 | tggggagcgtcgagagctcgagcaggtgtgctgaagagcagagaaagtgtgaaagggcagaagctgaa | 2580 |
| Dh | 2521 | tggggagcgtcgagagctcgagcaggtgtgctgaagagcagagaaagtgtgaaagggcagaagctgaa | 2580 |
| Qy | 2581 | gctgcgcagagatggttcagaggtgtgttccacagggccttgagaggtttctccgtctccctgtagagc | 2640 |
| Dh | 2581 | gctgcgcagagatggttcagaggtgtgttccacagggccttgagaggtttctccgtctccctgtagagc | 2640 |
| Qy | 2641 | ctcttctacctctctccctgctctcgagagaaagaaagctcaatctcaatcgaaagagagtagcattc | 2700 |
| Dh | 2641 | ctcttctacctctctccctgctctcgagagaaagaaagctcaatctcaatcgaaagagagtagcattc | 2700 |
| Qy | 2701 | ataaagctcagctgtataaaatcccaaggtgtgtgcatgtgttctctctccatcgaaagcctttat | 2760 |
| Dh | 2701 | ataaagctcagctgtataaaatcccaaggtgtgtgcatgtgttctctctccatcgaaagcctttat | 2760 |
| Qy | 2761 | ttaaatgggaaataatagaaagcagagcccatcttccctagagccggttaaatctccagagaaagagagac | 2820 |
| Dh | 2761 | ttaaatgggaaataatagaaagcagagcccatcttccctagagccggttaaatctccagagaaagagagac | 2820 |
| Qy | 2821 | tggagctctctctctctcaatgctctctcgtggcaactatcagccctgtgtgtgagcttggtcta | 2880 |
| Dh | 2821 | tggagctctctctctctcaatgctctctcgtggcaactatcagccctgtgtgtgagcttggtcta | 2880 |
| Qy | 2881 | tgcgaagacgtctcgaaaacctctggaatccagagagactcggttctctctctgtgcttgccact | 2940 |
| Dh | 2881 | tgcgaagacgtctcgaaaacctctggaatccagagagactcggttctctctctgtgcttgccact | 2940 |
| Qy | 2941 | ggttctgctgctgagacgtcgaggaagtgatctctctctctctctctctctgagcatatgcttctgcct | 3000 |
| Dh | 2941 | ggttctgctgctgagacgtcgaggaagtgatctctctctctctctctctctgagcatatgcttctgcct | 3000 |
| Qy | 3001 | ataaagagccctctgacgtctcgttctctgtgtaacaacatccctctgtaatctctctcgagaggg | 3060 |
| Dh | 3001 | ataaagagccctctgacgtctcgttctctgtgtaacaacatccctctgtaatctctctcgagaggg | 3060 |
| Qy | 3061 | ggagctctgagagagggaaagagagcagagagctgagagagctcgagccaaagggagaggtcgagag | 3120 |
| Dh | 3061 | ggagctctgagagagggaaagagagcagagagctgagagagctcgagccaaagggagaggtcgagag | 3120 |
| Qy | 3121 | ggacacggagagggcagaaagctgtgggtgtctctcatcaggtccctcaatgtgtatccagtcagagctc | 3180 |
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AC V51365;
XX 27-OCT-1998 (first entry)
XX Human TIGR promoter mutant TIGRmt4 DNA.
XX TIGR: trabecular meshwork induced glucocorticoid response protein; human;
XX diagnosis: glaucoma; polymorphism; steroid sensitivity; mutant; ss.
XX Homo sapiens.
OS Synthetic.
FH Key Location/Qualifiers
FT mutation 4256
FT /tag= a
FT /note= "Wild-type A is replaced by G"
PN W09832850-A1.
XX 30-JUL-1998.
PD 09-JAN-1998; 98WO-US00468.
PE 26-SEP-1997; 97US-0938669.
PR 28-JAN-1997; 97US-0791154.
XX (REGC) UNIV CALIFORNIA.
XX Chen H, Chen P, Nguyen TD, Polansky JR;
PI WPI; 1998-427946/36.
XX Use of TIGR nucleic acid sequences - used for, e.g. developing
PT products for diagnosis, prognosis and treatment of glaucoma
XX Disclosure; Fig 2; 105pp; English.
XX This sequence is a trabecular meshwork induced glucocorticoid response
XX protein (TIGR) promoter mutant, TIGRmt4, which is used in a method for
XX diagnosing glaucoma in a patient. The method involves the detection of
XX polymorphisms whose presence is predictive of a mutation affecting TIGR
XX response in the patient and can be diagnostic of glaucoma or steroid
XX sensitivity. Base substitutions and base additions upstream of and within
XX TIGR exons can also be used to diagnose glaucoma.
SQ Sequence 5300 BP; 1481 A; 1152 C; 1236 G; 1431 T; 0 other;

Query Match 99.5%; Score 5244.8; DB 19; Length 5300;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 5268; Conservative 0; Mismatches 2; Indels 2; Gaps 2;

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OY 61 tctctataaactgatatgctcccaatcggatgtatgtctcttggcagagatgataagaatca 120
DB 61 tctctataaactgatatgctcccaatcggatgtatgtctcttggcagagatgataagaatca 120
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DB 121 ggaagaagaagatcaccagtttagcagaagtgtccagagctgtctgtctctattttagtga 180
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DB 181 cagaatgtctctcctgacagaagctattctcaggaacaacatcacatccaatatgttaaatc 240
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DB 301 gagagcaataatgatgaataaataaactttcccttcttcttaatttcaggaaaaaatg 360
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DB 361 atgagagccaaaataatcaatgaataagaagaacagctccagaaaaaagatgttccaaatgg 420
OY 421 taattagatattgttcccttgggaagaagaccccatgtgaagcttgaatgggaatggga 480
DB 421 taattagatattgttcccttgggaagaagaccccatgtgaagcttgaatgggaatggga 480
OY 481 aaacgtcaaaagcatgacatcgaatcccaagtgtgataatcttaaaaaaccagat 540
DB 481 aaacgtcaaaagcatgacatcgaatcccaagtgtgataatcttaaaaaaccagat 540
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DB 1321 acctgagctcactgcaaaccttcgctcccaaggttcaagaatcttcctcttccagctcc 1380
OY 1381 cgcgtacgtggatctacaagcgacagcccgctaaattttgtatgtttagtagagaatgg 1440
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[illegible]

[illegible]

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| Qy | 4740 | gaggggggaaactctbcbgcagctctctataagaatgctctcccttgagacctggtatggctgct | 4799 |
| Db | 4740 | gaggggggaaactctgcgcctctctataagaatgctctcccttgagacctggtatggctgct | 4799 |
| Qy | 4800 | ccctgtgtctctgctgctgctgttatctttctctgctccctgctctacgtctctaaaggactgtt | 4859 |
| Db | 4800 | ccctgtgtctctgctgctgctgttatctttctctgctccctgctctacgtctctaaaggactgtt | 4859 |
| Qy | 4860 | tgaattcccaagttctcagcaatagtgcctgagcacaagtgacaggtcttccaaatgattgtcaga | 4919 |
| Db | 4860 | tgaattcccaagttctcctctagctatgtgccttgagcacaagtgacaggtcttccaaatgattgtcaga | 4919 |
| Qy | 4920 | gtgaaatgaaatabaaactagaataatactctgttgaatacagcacaccagtagtctctg | 4979 |
| Db | 4920 | gtgaaatgaaatabaaactagaataatactctgttgaatacagcacaccagtagtctctg | 4979 |
| Qy | 4980 | gtgtaaatgtgtgtgtacgt | 5039 |
| Db | 4980 | gtgtaaatgtgtgtgtacgt | 5039 |
| Qy | 5040 | ataagaactacttatttgggtatgt | 5099 |
| Db | 5040 | ataagaactacttatttgggtatgt | 5099 |
| Qy | 5100 | ccaaacagactctcgggaagttattttctcaagaatcttgcctgtgcagcgtgtgaaggaaaccc | 5159 |
| Db | 5100 | ccaaacagactctcgggaagttattttctcaagaatcttgcctgtgcagcgtgtgaaggaaaccc | 5159 |
| Qy | 5160 | ccctgtgtcaagcccccaaccagcctcaagctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt | 5219 |
| Db | 5160 | ccctgtgtcaagcccccaaccagcctcaagctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt | 5219 |
| Qy | 5220 | ggtctcccaatataataaacctctctgtgaagctctgggtacgtgacagcagaag | 5271 |
| Db | 5220 | ggtctcccaatataataaacctctctgtgaagctctgggtacgtgacagcagaag | 5271 |

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| RESULT | 6 | |
| ID | V51366 | |
| XX | V51366 standard; DNA; 5300 BP. | |
| XX | | |
| AC | V51366; | |
| XX | | |
| DT | 27-OCT-1998 | (first entry) |
| XX | | |
| DE | Human TIGR promoter mutant TIGRm5 DNA. | |
| XX | | |
| KW | TIGR; trabecular meshwork induced glucocorticoid response protein; human; | |
| KW | diagnosis; glaucoma; polymorphism; steroid sensitivity; mutant; ss. | |
| XX | | |
| OS | Homo sapiens. | |
| OS | Synthetic. | |
| XX | | |
| EH | Key | Location/Qualifiers |
| FT | mutation | 4262 |
| FT | | /*lag" a |
| XX | | /note="Wild-type G is replaced with A" |
| PN | W09832850-A1. | |
| XX | | |
| PD | 30-JUL-1998. | |
| XX | | |
| PF | 09-JAN-1998; | 98WO-U500468. |
| XX | | |
| PR | 26-SEP-1997; | 97US-0938669. |
| PR | 28-JAN-1997; | 97US-0791154. |
| XX | | |
| PA | (REGC) UNIV CALIFORNIA. | |
| XX | | |
| PI | Chen H, Chen P, Nguyen TD, Polansky JR; | |

XX WPI: 1998-427946/36.
XX Use of TIR nucleic acid sequences - used for, e.g. developing
PT products for diagnosis, prognosis and treatment of glaucoma
XX
PS Disclosure: Fig 2: 105pp: English.
XX
CC This sequence is a trabecular meshwork induced glucocorticoid response
CC protein (TIGR) promoter mutant, TIGRm5, which is used in a method for
CC diagnosing glaucoma in a patient. The method involves the detection of
CC polymorphisms whose presence is predictive of a mutation affecting TIGR
CC response in the patient and can be diagnostic of glaucoma or steroid
CC sensitivity. Base substitutions and base additions upstream of and within
CC TIGR exons can also be used to diagnose glaucoma.
XX
SO Sequence 5300 BP: 1483 A: 1152 C: 1234 G: 1431 T: 0 other:

Query Match 99.5%; Score 5244.8; DB 19; Length 5300;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 5268: Conservative 0; Mismatches 2; Indels 2; Gaps 2;

QY 1 atcttcttcagtttaccctcaggagctatataatgaatgaataaaccatgtgaag 60
Db 1 atcttcttcagtttaccctcaggagctatataatgaatgaataaaccatgtgaag 60
QY 61 tccctaaactcgtataagccctcattcggatgtatgtcttttggcagatgataaagatca 120
Db 61 tccctaaactcgtataagccctcattcggatgtatgtcttttggcagatgataaagatca 120
QY 121 ggaagaagaatataccaggttagcagaatgtccagagctgtcgtccttattttatga 180
Db 121 ggaagaagaatataccaggttagcagaatgtccagagctgtcgtccttattttatga 180
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[illegible]

| | | | |
|-----------------------|---|--|---------------------|
| Dd | 5100 | ccaacagactctcgtgaaggatttttcttcctaagaatctgctgcgcgcgtlgaaggcaacc | 5159 |
| Oy | 5160 | cctcgctgcacaagcccccacccagctcacgltggccacctctgtcttcccccatgaaggct | 5219 |
| | | | |
| Dd | 5160 | cctcgctgcacaagcccccacccagctcacgltggccacctctgtcttcccccatgaaggct | 5219 |
| Oy | 5220 | ggctccccagtatatataaacctctcttggaagctcgggatgaagccagcaagg | 5271 |
| | | | |
| Dd | 5220 | ggctccccagtatatataaacctctcttggaagctcgggatgaagccagcaagg | 5271 |
| <hr/> | | | |
| RESULT 7 | | | |
| ID | V51367 | V51367 standard; DNA: 5300 BP. | |
| AC | V51367; | | |
| DT | 27-OCT-1998 | (first entry) | |
| DE | Human TIGR promoter variant TIGRSv1 DNA. | | |
| KW | TIGR: trabecular meshwork induced glucocorticoid response protein; human: | | |
| KW | diagnosis; glaucoma; polymorphism; steroid sensitivity; mutant; ss. | | |
| OS | Homo sapiens. | | |
| OS | Synthetic. | | |
| XX | | Location/Qualifiers | |
| FT | Key | 4406 | |
| FT | mutation | /tag= a | |
| FT | | /note= "Wild-type A is replaced by G" | |
| FN | MO9832850-AI. | | |
| PD | 30-JUL-1998. | | |
| PF | 09-JAN-1998; | 98NC-US00468. | |
| PR | 26-SEP-1997; | 97US-0938669. | |
| PR | 28-JAN-1997; | 97US-0791154. | |
| PA | (REGC) UNIV CALIFORNIA. | | |
| P1 | Chen H, Chen P, Nguyen TD, Polansky JR; | | |
| DR | WPI: 1998-427946/36. | | |
| PT | Use of TIGR nucleic acid sequences - used for, e.g. developing | | |
| PT | products for diagnosis, prognosis and treatment of glaucoma | | |
| PS | Disclosure; Fig 2: 105pp; English. | | |
| CC | This sequence is a trabecular meshwork induced glucocorticoid response | | |
| CC | protein (TIGR) promoter variant, TIGRSv1, which is used in a method for | | |
| CC | diagnosing glaucoma in a patient. The method involves the detection of | | |
| CC | polymorphisms whose presence is predictive of a mutation affecting TIGR | | |
| CC | response in the patient and can be diagnostic of glaucoma or steroid | | |
| CC | sensitivity. Base substitutions and base additions upstream of and within | | |
| CC | TIGR exons can also be used to diagnose glaucoma. | | |
| SO | Sequence 5300 BP; 1481 A; 1152 C; 1236 G; 1431 T; 0 other; | | |
| <hr/> | | | |
| Query Match | 99.5%; | Score 5244.8; | DB 19; Length 5300; |
| Best Local Similarity | 99.9%; | Pred No. 0; | |
| Matches 5266; | Conservative 0; | Mismatches 2; | Indels 2; Gaps 2 |
| Oy | 1 attcttgtcagttaccctcgaagcgcattatgaatgaatgagataaccaatgtgaag | 60 | |
| | | | |
| Dd | 1 attcttgtcagttaccctcgaagcgcattatgaatgaatgagataaccaatgtgaag | 60 | |
| | | | |
| Oy | tctcataactgtatagcctccatcgcattggaatgtaagtctcttggcagagatgaaagaatca | 120 | |
| | | | |

Dh 61 tccataaactgtatagccctccattccgatagtatcttctggcagagatataaagatca 120
Oy 121 ggaagaaagagatcatcagcttagcgaagctgtacagcgtgtctgtcttatctttagtga 180
Dh 121 ggaagaaagagatcatcagcttagcgaagctgtacagcgtgtctgtcttatctttagtga 180
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Dh 181 cgaagcttgcctctgacaaagactatctctcaggaagaaacatccatccaaatagtataac 240
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Oy 1801 ttcacatttggggcaccatctgtgtgtgataagggaggggcataccccagaactcct 1860
Dh 1801 ttcacatttggggcaccatctgtgtgtgataagggaggggcataccccagaactcct 1860
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Dh 1861 tgaagcccccggcagaaggttctctctccagctggggagccctgcagagcaccgggtcc 1920
Oy 1921 ttgggttctctggcaacccctgcagcccgctgcagctgtgttctgtatcaactcttag 1980
Dh 1921 ttgggttctctggcaacccctgcagcccgctgcagctgtgttctgtatcaactcttag 1980
Oy 1981 gacctgttgccttctatcttctgtgtgatacctgtcatctacccaggtcatctgaacaat 2040
Dh 1981 gacctgttgccttctatcttctgtgtgatacctgtgtcatctacccaggtcatctgaacaat 2040
Oy 2041 tatgtgactctatactctgcagacaacagagaacaaatvggtgagcaaaagctactctc 2100
Dh 2041 tatgtgactctatactctgcagacaacagagaacaaatvggtgagcaaaagctactctc 2100
Oy 2101 cctaactctgtgaggttgagcaatttctcaatggaaagcgtgcagaaagaaaaatcaatggca 2160
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Dh 2221 agcatccttaacaaagcaccctcccttagcggccctctgtgcctccatctgtccggaggg 2280

| | | | |
|----|------|---|------|
| OY | 2281 | cccccaagcccgagtccttccaaagccctccctccatcaagtcagtcagtcgctc | 2340 |
| Db | 2281 | cccccaagcccgagtccttccaaagccctccctccatcaagtcagtcagtcgctc | 2340 |
| OY | 2341 | gctccgctcccgctcgaaatctgctccctgctgcaatctcgaaagctcgaaagctccaaagct | 2400 |
| Db | 2341 | gctccgctcccgctcgaaatctgctccctgctgcaatctcgaaagctcgaaagctccaaagct | 2400 |
| OY | 2401 | ccgaagaagaaatcgaaagagaaagaaatcagtcctaaacggaaagaaatctgaaagagaaatgcttcc | 2460 |
| Db | 2401 | ccgaagaagaaatcgaaagagaaagaaatcagtcctaaacggaaagaaatctgaaagagaaatgcttcc | 2460 |
| OY | 2461 | ctcgaagagaaagagggcctcccaagctccaaagaaatctcgaagagctgagagatctgcaagagag | 2520 |
| Db | 2461 | ctcgaagagaaagagggcctcccaagctccaaagaaatctcgaagagagctgagagagctgcaagagag | 2520 |
| OY | 2521 | ctgaggaagctcgagggctcgaaagggctgctcgaaagagcagaagagctgaaagagcagaagctcga | 2580 |
| Db | 2521 | ctgaggaagctcgagggctcgaaagggctgctcgaaagagcagaagagctgaaagagcagaagctcga | 2580 |
| OY | 2581 | gctcccccgaagatgctcagtcgctcgaacggggctcgagagagcttcctcgctccctctgagcc | 2640 |
| Db | 2581 | gctcccccgaagatgctcagtcgctcgaacggggctcgagagagcttcctcgctccctctgagcc | 2640 |
| OY | 2641 | ctcttcacctctctcctgctcgagagaaagaaatctcaatccagaaagatgcaagcttc | 2700 |
| Db | 2641 | ctcttcacctctctcctgctcgagagaaagaaatctcaatccagaaagatgcaagcttc | 2700 |
| OY | 2701 | ataaagctcagctgtgtaaatctcagaagctgagcaatgagcttcctccacgaagagcccttat | 2760 |
| Db | 2701 | ataaagctcagctgtgtaaatctcagaagctgagcaatgagcttcctccacgaagagcccttat | 2760 |
| OY | 2761 | ctaaatgagaaatcagaaagagaaagcctcaatctccaaagccgttcaatccagaaagaaatgagc | 2820 |
| Db | 2761 | ctaaatgagaaatcagaaagagaaagcctcaatctccaaagccgttcaatccagaaagaaatgagc | 2820 |
| OY | 2821 | ctgagctctctctctcaatgctctctctcgagcaactcaagccctgctgagactgagctta | 2880 |
| Db | 2821 | ctgagctctctctctcaatgctctctctcgagcaactcaagccctgctgagactgagctta | 2880 |
| OY | 2881 | ctgcaagagcggcgaaagaaacctctgaaatcagaagagctcggttctctcttcggtctcgcaat | 2940 |
| Db | 2881 | ctgcaagagcggcgaaagaaacctctgaaatcagaagagctcggttctctcttcggtctcgcaat | 2940 |
| OY | 2941 | ggtctgagctgagcaacggctggagcaagtgctctctctccctctggagcaatgctctctcact | 3000 |
| Db | 2941 | ggtctgagctgagcaacggctggagcaagtgctctctctccctctggagcaatgctctctcact | 3000 |
| OY | 3001 | ataaagaacccctcgagctctcgctgctctcgagaaacatctccctgctgactctctctgtagaggg | 3060 |
| Db | 3001 | ataaagaacccctcgagctctcgctgctctcgagaaacatctccctgctgactctctctgtagaggg | 3060 |
| OY | 3061 | ggaagctcgaaaggggaaagggcgcaagctcgagcaagctcgagcccaagagggaggtgaaaggg | 3120 |
| Db | 3061 | ggaagctcgaaaggggaaagggcgcaagctcgagcaagctcgagcccaagagggaggtgaaaggg | 3120 |
| OY | 3121 | ggaacgaagaaagcagaagcagaagctcgaggtgctcgcaatcgactctcaatcgatcaacgcaagctc | 3180 |
| Db | 3121 | ggaacgaagaaagcagaagcagaagctcgaggtgctcgcaatcgactctcaatcgatcaacgcaagctc | 3180 |
| OY | 3181 | cagaagccgaagagccacaatgctctcgaagaaagctcgaatgaaaccaaagccacaatcttcc | 3240 |
| Db | 3181 | cagaagccgaagagccacaatgctctcgaagaaagctcgaatgaaaccaaagccacaatcttcc | 3240 |
| OY | 3241 | ctccctaaagcataagcaatgagcattctgccaataaacccaagaaatgagcagagactaaatgct | 3300 |
| Db | 3241 | ctccctaaagcataagcaatgagcattctgccaataaacccaagaaatgagcagagactaaatgct | 3300 |
| OY | 3301 | ggtagcctcttgcccgagatctcaaaaactctggccagaagcagaagctgagaaatgccaagagatg | 3360 |
| Db | 3301 | ggtagcctcttgcccgagatctcaaaaactctggccagaagcagaagctgagaaatgccaagagatg | 3360 |
| OY | 3361 | ctaaactcttcaacccctgaaacgaagccccaagcagctcgaagagtgactctgtaacgaatg | 3420 |

[illegible]

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Db 4500 aatttgaataattgtaatacatattcatattcatattgtttccttgytaattatatt 4559
Oy 4560 tatataattgaaaacaactcttcgtagaagaagttccccaagattccacaatgaagttcttg 4619
Db 4560 tatataattgaaaacaactcttcgtagaagaagttccccaagattccacaatgaagttcttg 4619
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Db 4620 gcatgcacacacacagaglaagaactgatttaagggttaacatgtacattgtgtcctgaag 4679
Oy 4680 atgcagaactgaaattagaagaattcctcccaagatacacagttgttttaagctaaaggtt 4739
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Db 4740 gaaggagggaatactgcgcgtctctataaggaaatgtctcccccggagcctgtgaaggtcgtc 4799
Oy 4800 ccttgyttctcgtcgtcgttattttctctcgtcctcgtcgaagcttaagaagcttgtt 4859
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Db 4980 gtgtaagtgctgtcgaagtgctgt 5039
Oy 5040 ataggaactatattctgt 5099
Db 5040 ataggaactatattctgt 5099
Oy 5100 ccaaaagaactcttggaagaagtattttcttaagaatctgtcttggaaggttaagaagctcc 5159
Db 5100 ccaaaagaactcttggaagaagtattttcttaagaatctgtcttggaaggttaagaagctcc 5159
Oy 5160 cccctgtgcacagcccaacacagcctcagctgtgcacacctcgtctctcccatgaaaggtc 5219
Db 5160 cccctgtgcacagcccaacacagcctcagctgtgcacacctcgtctctcccatgaaaggtc 5219
Oy 5220 ggcctcccgatataataaactcctctggaagcctgggcatgagccgcaagg 5271
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RESULT 8
V51364
ID V51364 standard; DNA: 5304 BP.
XX V51364:
XX
XX
DT 27-OCT-1998 (first entry)
XX
DE Human TIGR promoter mutant TIGRmt3 DNA.
XX
XX TIGR: trabecular meshwork induced glucocorticoid response protein; human;
KM diagnosis; glaucoma; polymorphism; steroid sensitivity; mutant; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
XX Key Location/Qualifiers
FH mutation 4997..5002
FT

FT /*tag= a
FT /note= "Wild-type TG is replaced with TGTGTG"
PN WO9832850-A1.
XX
XX 30-JUL-1998.
PD
XX
XX 09-JAN-1998; 98MO-US00468.
PF
XX 26-SEP-1997; 97US-0938669.
PR 28-JAN-1997; 97US-0791154.
XX
XX (REGC) UNIV CALIFORNIA.
PI Chen H, Chen P, Nguyen TD, Polansky JR;
XX
XX WPI; 1998-427946/36.
DR
XX
XX
XX Use of TIGR nucleic acid sequences - used for, e.g. developing
PT products for diagnosis, prognosis and treatment of glaucoma
XX
XX
XX Disclosure; Fig 2; 105pp; English.
PS
XX This sequence is a trabecular meshwork induced glucocorticoid response
CC protein (TIGR) promoter mutant, TIGRmt3, which is used in a method for
CC diagnosing glaucoma in a patient. The method involves the detection of
CC polymorphisms whose presence is predictive of a mutation affecting TIGR
CC response in the patient and can be diagnostic of glaucoma or steroid
CC sensitivity. Base substitutions and base additions upstream of and within
XX TIGR exons can also be used to diagnose glaucoma.
XX
XX Sequence 5304 BP: 1482 A; 1152 C; 1237 G; 1433 T; 0 other:
SO

Query Match 99.3%; Score 5232.4; DB 19; Length 5304;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 5269; Conservative 0; Mismatches 1; Indels 6; Gaps 3:
Oy 1 attcttgctcaagttatccctcagggcctatcatgaataatgaatgataaccatgtgaag 60
Db 1 attcttgctcaagttatccctcagggcctatcatgaataatgaatgataaccatgtgaag 60
Oy 61 tccataaactgatatgcccacatcggatgtatgtctcttggaagatgataaagatca 120
Db 61 tccataaactgatatgcccacatcggatgtatgtctcttggaagatgataaagatca 120
Oy 121 ggaagaaggagatccacgttaagcaagtgctccaggctgtctgtctatatttagta 180
Db 121 ggaagaaggagatccacgttaagcaagtgctccaggctgtctgtctatatttagta 180
Oy 181 cagatgtgtctctcgtgcagaagttatcttcagaagaatacacaatcatatgtgtaattc 240
Db 181 cagatgtgtctctcgtgcagaagttatcttcagaagaatacacaatcatatgtgtaattc 240
Oy 241 catcaaacagagctaaagaacacagatgagatggcactctgcgaagaaatgtccag 300
Db 241 catcaaacagagctaaagaacacagatgagatggcactctgcgaagaaatgtccag 300
Oy 301 gagaagcaaatatgatgaaataaactcttcctctgttttttaattccagaaaaatg 360
Db 301 gagaagcaaatatgatgaaataaactcttcctctgttttttaattccagaaaaatg 360
Oy 361 atgagaccacaaatcaatgaataagaaaaacagctcagaaaaaagatgtttccaaattg 420
Db 361 atgagaccacaaatcaatgaataagaaaaacagctcagaaaaaagatgtttccaaattg 420
Oy 421 taattaaattgttctccttggaagagacccatcgtgagcttgatgggaaattggaa 480
Db 421 taattaaattgttctccttggaagagacccatcgtgagcttgatgggaaattggaa 480
Oy 481 aaacgtcaaaagcatgactgatacagatcccaagtgatattatttttaaaaccagat 540
Db 481 aaacgtcaaaagcatgactgatacagatcccaagtgatattatttttaaaaccagat 540

| | | | |
|----|------|--|------|
| Oy | 541 | ggcctacctctggggagagcgaagtcacggaagtcagtgtaacgaagacataacataac | 600 |
| Db | 541 | ggcctacctctggggagagcgaagtcacggaagtcagtgtaacgaagacataacataac | 600 |
| Oy | 601 | agcaaaatcaaaattccgcgaatgcagagaggaanaatgaggatctggaaagcttcatac | 660 |
| Db | 601 | agcaaaatcaaaattccgcgaatgcagagaggaanaatgaggatctggaaagcttcatac | 660 |
| Oy | 661 | agtgattagcagcttgcacatgtgtcgcacaacctcccgctcataccaggggaacaaa | 720 |
| Db | 661 | agtgattagcagcttgcacatgtgtcgcacaacctcccgctcataccaggggaacaaa | 720 |
| Oy | 721 | attgcactggtgcttaagccttggaacttccaagggaaatatgtanaaacggaagcaaaacaaa | 780 |
| Db | 721 | attgcactggtgcttaagccttggaacttccaagggaaatatgtanaaacggaagcaaaacaaa | 780 |
| Oy | 781 | gacacatgtctaaagagcaaccagaacatctggagaccttcaaaacaaacagtgccctcagca | 840 |
| Db | 781 | gacacatgtctaaagagcaaccagaacatctggagaccttcaaaacaaacagtgccctcagca | 840 |
| Oy | 841 | gggacacctgagagcaattgcctttaagaaagcgcaatttcttaaggaaatccttaagaaatc | 900 |
| Db | 841 | gggacacctgagagcaattgcctttaagaaagcgcaatttcttaaggaaatccttaagaaatc | 900 |
| Oy | 901 | cttgaaagatctcttgaaattttaacattttaagatctaaacaaatacgagatgtcataacag | 960 |
| Db | 901 | cttgaaagatctcttgaaattttaacattttaagatctaaacaaatacgagatgtcataacag | 960 |
| Oy | 961 | cttcagacaatgggtcccaattctataaagtctagacatacaagaagataacgtgtccagctcc | 1020 |
| Db | 961 | cttcagacaatgggtcccaattctataaagtctagacatacaagaagataacgtgtccagctcc | 1020 |
| Oy | 1021 | ggatagatgcagaatactatagaaatcacctgtgtcccatcctaacttcttcagaaatgatac | 1080 |
| Db | 1021 | ggatagatgcagaatactatagaaatcacctgtgtcccatcctaacttcttcagaaatgatac | 1080 |
| Oy | 1081 | tgctatagcctctcacacacagcgccgaatgtgtcttgacctacaacacactctacaaccaa | 1140 |
| Db | 1081 | tgctatagcctctcacacacagcgccgaatgtgtcttgacctacaacacactctacaaccaa | 1140 |
| Oy | 1141 | gtgcctcaacacatgtttaaagctgtcatctcatagatgcccatctacaatgtccacactccc | 1200 |
| Db | 1141 | gtgcctcaacacatgtttaaagctgtcatctcatagatgcccatctacaatgtccacactccc | 1200 |
| Oy | 1201 | tgctcagaccccatcccgctccacagagaagtcctcccaactctagactctgtcacaagatgt | 1260 |
| Db | 1201 | tgctcagaccccatcccgctccacagagaagtcctcccaactctagactctgtcacaagatgt | 1260 |
| Oy | 1261 | tacagcgcaagaagctccgttgtagggcttgtagggctgtgtcttaacacctcaactctgtagctcac | 1320 |
| Db | 1261 | tacagcgcaagaagctccgttgtagggcttgtagggctgtgtcttaacacctcaactctgtagctcac | 1320 |
| Oy | 1321 | accctgagctctcaactcgaacacctctgcctcccaaggtctcaagaacattccctgtctcagctccc | 1380 |
| Db | 1321 | accctgagctctcaactcgaacacctctgcctcccaaggtctcaagaacattccctgtctcagctccc | 1380 |
| Oy | 1381 | cgcgtaagcttgtagctacagcgacagcgcccgctaaatttctgtatctgtatagatagatggg | 1440 |
| Db | 1381 | cgcgtaagcttgtagctacagcgacagcgcccgctaaatttctgtatctgtatagatagatggg | 1440 |
| Oy | 1441 | gtttcaacacatctttagcccgctgtctcttgaaacctctgaaactaaggctgataccaacacatc | 1500 |
| Db | 1441 | gtttcaacacatctttagcccgctgtctcttgaaacctctgaaactaaggctgataccaacacatc | 1500 |
| Oy | 1501 | agccctccctaaagatctctggagcttaacagcaatgataccgctcgcccgccgaagaggtcaatgt | 1560 |
| Db | 1501 | agccctccctaaagatctctggagcttaacagcaatgataccgctcgcccgccgaagaggtcaatgt | 1560 |
| Oy | 1561 | ctaaataagaaataactctggaatgttctaaataacaaacaaagaaacaaagactgtga | 1620 |
| Db | 1561 | ctaaataagaaataactctggaatgttctaaataacaaacaaagaaacaaagactgtga | 1620 |

[illegible]

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Db 3781 taagaccaaacagattcaagcctaggtctgtgactaatgtatgtgtttttgaaaat 3840
|||||

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QY 4200 ggaattattaaacttaagctcagaagcctgtgaaatttgaatgaggaaaaaatataactt 4259
Db 4200 ggaattattaaacttaagctcagaagcctgtgaaatttgaatgaggaaaaaatataactt 4259
QY 4260 ttgttttcaacacctctaaactaaacttaacatttatcccatctggcaatagccataa 4319
Db 4260 ttgttttcaacacctctaaactaaacttaacatttatcccatctggcaatagccataa 4319
QY 4320 actcaaaagtgttaataacagtaactgtgtatgttgcattacaaatagaatcaacagacat 4379
Db 4320 actcaaaagtgttaataacagtaactgtgtatgttgcattacaaatagaatcaacagacat 4379
QY 4380 ttatactatataaagttgttgcaagatacgtgtgaatgaaatatttactacaaact 4439
Db 4380 ttatactatataaagttgttgcaagatacgtgtgaatgaaatatttactacaaact 4439
QY 4440 accttgaatataagacctccgcgtgcagatctgttttcaacataataataaacctgttaa 4499
Db 4440 accttgaatataagacctccgcgtgcagatctgttttcaacataataataaacctgttaa 4499
QY 4500 aatttgaataatttgaataabcatattcatltaacttgttctccttgaatacatabact 4559
Db 4500 aatttgaataatttgaataabcatattcatltaacttgttctccttgaatacatabact 4559
QY 4560 tatatatattgaaanaacttctctgagaagaaggtccccaagattccacaatgaaagttcttg 4619
Db 4560 tatatatattgaaanaacttctctgagaagaaggtccccaagattccacaatgaaagttcttg 4619
QY 4620 gcatgacacacacagagtaagaactgatttgaaggctaaacatgtgacatgtggcctgag 4679
Db 4620 gcatgacacacacagagtaagaactgatttgaaggctaaacatgtgacatgtggcctgag 4679
QY 4680 atgcaagacttgaataatagaagaattctcccaagaatacacagatgttcttaaagctaggggt 4739
Db 4680 atgcaagacttgaataatagaagaattctcccaagaatacacagatgttcttaaagctaggggt 4739
QY 4740 gaagggggaaatctgcgcgtctcataggaatgtctccctggagcctgtgtagggtgctgt 4799
Db 4740 gaagggggaaatctgcgcgtctcataggaatgtctccctggagcctgtgtagggtgctgt 4799
QY 4800 ccttctgtcttgctggctgtgtatatttctctgtctccctgttaagagctgtt 4859
Db 4800 ccttctgtcttgctggctgtgtatatttctctgtctccctgttaagagctgtt 4859
QY 4860 tgaatctccagttccttagcaatgtgcctggcacaaggtctctcaatgagtcttcagag 4919
Db 4860 tgaatctccagttccttagcaatgtgcctggcacaaggtctctcaatgagtcttcagag 4919
|||||
```

[illegible]

RESULT 9
 ID 237968 standard: DNA: 2800 BP.
 AC 237968:
 DT 07-FEB-2000 (first entry)
 DE Human GLCIA gene exon 1 and flanking sequences.
 KW GLIAComa: PCR amplification: primary open wide angle gliucoma;
 KW GLCIA gene: exon; human; ss.
 OS Homo sapiens.
 PN W09951779-A2.
 PD 14-OCT-1999.
 PF 07-APR-1999: 99WO-US07671.
 PR 07-APR-1998: 98US-0056285.
 PA (IOWA) UNIV IOWA RES FOUND.
 PI Stone EM, Sheffield VC, Alward LWM, Fingert J;
 DR MPI: 2000-022956/02.
 PT Determination of a predisposition to gliucoma by analysing mutations in
 PT the GLCIA gene -
 PS Disclosure: Fig 1A; 137Pp: English.
 CC The invention relates to a method for the determination of a
 CC predisposition to gliucoma. The method comprises amplifying a GLCIA gen
 CC with a primer pair selected from the sequences shown in 237981-238008.
 CC The primers are used to determine whether a subject has or has the
 CC potential to develop primary open wide angle gliucoma. The present
 CC sequence represents the human GLCIA gene exon 1 and flanking sequences.
 Q0 Sequence 2800 BP: 781 A: 588 C: 673 G: 758 T: 0 other:

| | | | | |
|-----------------------|--------------|---------------|---------------|--------------|
| Query Match | 34.28; | Score 1804.4; | DB 21; | Length 2800; |
| Best Local Similarity | 99.8%; | Pred. No. 0; | | |
| Matches 1838; | Conservative | 0; | Mismatches 1; | Indels 3; |
| | | | Gaps | 3; |

| | | | |
|----|------|---|------|
| Oy | 3431 | agcgagagggagggagaaagaaagagggagatggtctatgagccaggaagaaagatctat | 3490 |
| Db | 1 | agcgagagggagggagag -aaagagagggatggtctatgagccaggaagaaagatctat | 59 |
| Oy | 3491 | tcaagggcagcggaatctgacccagagatcatagtccaagctgacttgggtcttagag | 3550 |
| Db | 60 | tcaagggcagcggaatctgacccagagatcatagtccaagctgacttgggtcttagag | 119 |
| Oy | 3551 | gcagggcctatctgtgggggaaaaaaatcagttccaaggaattggggagactgtttct | 3610 |
| Db | 120 | gcagggcctatctgtgggggaaaaaaatcagttccaaggaattggggagactgtttct | 179 |
| Oy | 3611 | aatacatatttcccttcaagctgagtaattccgagcaagctcacaaggtagtaactg | 3670 |
| Db | 180 | aatacatatttcccttcaagctgagtaattccgagcaagctcacaaggtagtaactg | 239 |
| Oy | 3671 | aggcgtgaagatctcctagtctctccttattagaacctttttctctgtggagttaga | 3730 |
| Db | 240 | aggcgtgaagatctcctagtctctccttattagaacctttttctctgtggagttaga | 299 |
| Oy | 3731 | gcacaaaggccaatccggttctctttcaacaggaagaaacatccctcaaggttagaacca | 3790 |
| Db | 300 | gcacaaaggccaatccggttctctttcaacaggaagaaacatccctcaaggttagaacca | 359 |
| Oy | 3791 | cagattcaagccttagtctgtctgacatatagtttgtttttgaaaaatcatcttcagc | 3850 |
| Db | 360 | cagattcaagccttagtctgtctgacatatagtttgtttttgaaaaatcatcttcagc | 419 |
| Oy | 3851 | atgtttactatctatctcagaaaaatgagacataacccttttgcaagctgtagaaaaa | 3910 |
| Db | 420 | atgtttactatctatctcagaaaaatgagacataacccttttgcaagctgtagaaaaa | 479 |
| Oy | 3911 | cccaattctaaatgtctccaagttcaaggttaactacgtgcagaaaccaatcaaa -aagaaataga | 3969 |
| Db | 480 | cccaattgtaaatgtctccaagttcaaggttaactacgtgcagaaaccaatcaaaataga | 539 |
| Oy | 3970 | tctttaagcgaacgtgttcttccacacttggaggtggtctgcgaaggcagtttgaa | 4029 |
| Db | 540 | tctttaagcgaacactgtgttcttccaa -tctggaggtgggtctgtgcgaaggcagtttgaa | 598 |
| Oy | 4030 | ataatttactcaagatctgacagctgtgtgtgtatcaacaataagttgtctcaag | 4089 |
| Db | 599 | ataatttactcaagatctgacagctgtgtgtgtatcaacaacaataagttgtctcaag | 658 |
| Oy | 4090 | gcaatcatatttcaagtgtgcttaagaattcacttcgacagtttggatattatgtgct | 4149 |
| Db | 659 | gcaatcatatttcaagtgtgcttaagaattcacttctgacagtttggatattatgtgct | 718 |
| Oy | 4150 | attgacatttgcctttgttttttcccttgggtttattaatgttaagaaagagattata | 4209 |
| Db | 719 | attgacatttgcctttgttttttcccttgggtttattaatgttaagaaagagattata | 778 |
| Oy | 4210 | acctcagttccaagaagcgtgtgaatttgatagtaggaaaaaaatltcaatttgttttac | 4269 |
| Db | 779 | acctcagttccaagaagcgtgtgaatttgatagtaggaaaaaaatltcaatttgttttac | 838 |
| Oy | 4270 | caacttcaactaaatttaacattttatccattgtggaatagaagccataactcaagtg | 4329 |
| Db | 839 | caacttcaactaaatttaacattttatccattgtggaatagaagccataactcaagtg | 898 |
| Oy | 4330 | gtaataaagatgaactgtgattttgtatccaatgaataacagacattttatcat | 4389 |
| Db | 899 | gtaataaagatgaactgtgattttgtatccaatgaataacagacattttatcat | 958 |
| Oy | 4390 | attacagttgttgagatacgtgtgaagtgaatatltatctcaaaaactacttgaat | 4449 |
| Db | 959 | attacagttgttgagatacgtgtgaagtgaatatltatctcaaaaactacttgaat | 1018 |
| Oy | 4450 | tagacctctgcgtgacactgttttttaaacattataaanaaagttttaaattttga | 4509 |
| Db | 1019 | tagacctctgcgtgacactgttttttaaacattataaanaaagttttaaattttga | 1078 |

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Oy 4510 ttctgataatcattcatatcatatcttctctcttctgtaactatatttataattg 4569
    |||
Db 1079 ttctgataatcattcatatcttctcttcttcttcttctgtaactatatttataattg 1138
Oy 4570 aaacacattctctggaagagttcccccagattccacaaatgagttctctgcatgcac 4629
    |||
Db 1139 aaacacattctctggaagagttcccccagattccacaaatgagttctctgcatgcac 1198
Oy 4630 acacagatgaagaactgatttgaaggtcacttgaacttgaacttgaacttgaacttgaact 4689
    |||
Db 1139 acacagatgaagaactgatttgaaggtcacttgaacttgaacttgaacttgaacttgaact 1258
Oy 4690 gaattatgaagaacttctcccaagaatacacagattgttttaaaactgaggtgagggagaa 4749
    |||
Db 1259 gaattatgaagaacttctcccaagaatacacagattgttttaaaactgaggtgagggagaa 1318
Oy 4750 atctgcgcctctatagaagaatctctccctgagcctgtaaggtgctgctctgcttctc 4809
    |||
Db 1319 atctgcgcctctatagaagaatctctccctgagcctgtaaggtgctgctctgcttctc 1378
Oy 4810 tggctgcgcctgatttcttctctctctctctctctctctctctctctctctctctctca 4869
    |||
Db 1379 tggctgcgcctgatttcttctctctctctctctctctctctctctctctctctctctca 1438
Oy 4870 gtctctagatagtgctctgcaagtgctctctcaatgagatttgcagaatgagaa 4929
    |||
Db 1439 gtctctagatagtgctctgcaagtgctctctcaatgagatttgcagaatgagaa 1498
Oy 4930 atataaactagaataatcctctgttgaatacagacacacagtgagtcctggtgtaagt 4989
    |||
Db 1499 atataaactagaataatcctctgttgaatacagacacacagtgagtcctggtgtaagt 1558
Oy 4990 ggtctcgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 5049
    |||
Db 1559 ggtctcgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1618
Oy 5050 ttaattggggtatgggtgcaataattggatgtctctcttcaaaagaagaactcccaagaac 5109
    |||
Db 1619 ttaattggggtatgggtgcaataattggatgtctctcttcaaaagaagaactcccaagaac 1678
Oy 5110 tctctggaaggttatttctctaaagaatctctgcaagcgtgaagggcaacccctgtgac 5169
    |||
Db 1679 tctctggaaggttatttctctaaagaatctctgcaagcgtgaagggcaacccctgtgac 1738
Oy 5170 agcccaaccagcctcagctgagccactctgtctctcccaatgaaggtctgtctccag 5229
    |||
Db 1739 agcccaaccagcctcagctgagccactctgtctctcccaatgaaggtctgtctccag 1798
Oy 5230 tatataaactctctgagctcgagctcgagcattgagccagcaag 5271
    |||
Db 1799 tatataaactctctgagctcgagcattgagccagcaag 1840

RESULT 10
ID 063862 standard; cDNA: 283 BP.
XX
AC 063862:
XX
DT 29-JAN-1995 (first entry)
XX
DE AP2 sequence obtd. by PCR for tumour specific DNA.
XX
KW Arbitrary primers: AP-PCR; amplification: tumour cells; cancer;
XX insertions: deletions; ss.
XX
OS Synthetic.
XX
PN WO9411531-A.
XX
PD 26-MAY-1994.
XX
PF 12-NOV-1993; 93WO-US10904.
```

```
XX
PR 13-NOV-1992; 92US-0975737.
XX
PA (CALB-) CALIFORNIA INST BIOLOGICAL RES.
XX
PI Ionov Y, Malkhosyan S, McClelland M, Pelinado MA:
XX Perucho M, Welsh J;
XX
DR WPI: 1994-183529/22.
XX
PT Identification of tumour cells - by analysing DNA to determine
XX whether insertions or deletions have occurred in reiterated
XX sequences
XX
PS Disclosure: Page 52; 67pp; English.
XX
CC The sequence was obtd. by PCR with arbitrary PCR primers used to
XX detect insertions or deletions in DNA sequences. Such mutations are
XX markers of cancer so such primers can be used in the diagnosis of
XX cancer. esp. colorectal, stomach or pancreatic tumours.
XX See also Q63837-63.
XX
SQ Sequence 283 BP; 63 A; 77 C; 94 G; 49 T; 0 other;

Query Match 3.3%; Score 176.4; DB 15; Length 283;
Best Local Similarity 80.4%; Pred. No. 2e-31;
Matches 222; Conservative 0; Mismatches 46; Indels 8; Gaps 1;

Oy 1281 ggttgaaggtctgtgtcttctacacactgtaactgtctctacacactgagctcaact 1340
    |||
Db 276 GAGTCTCGCTCTGTGCCAGCGTAGAGTGGCGGATCGCTCACTGCACACT 217
Oy 1341 ctgcctccaggttcaagaatctccctgctcagccctcccgagctgagctggaccacagg 1400
    |||
Db 216 CCACCTCCCGGGTTCAAGGATTCCTGCTCACCCCTCCGAGTAGCTGGGATTAACAG 157
Oy 1401 cg-----cagcccgctaatcttctgattgttgaatgagatgggttcacacat 1452
    |||
Db 156 CCGCGGCCACACGCCCGGCTAATTTTGTATTAGTAGAGAGGGGTTTCACTATGT 97
Oy 1453 tagcccggtgtgtcttgaactcctgactcaggtgataccacacactcagctctctaaag 1512
    |||
Db 96 TGGCCAGGCTGTGTGAACCTCTGACCTCAGGTGATCCACCACCTGGCCTCCCAAG 37
Oy 1513 tgcctggtatcacagatgagtcacgcgcgcgcgc 1548
    |||
Db 36 TGCTGGATTACAGGTGTGACGCCACGCGCCAGCC 1

RESULT 11
ID 286967/c 286967 standard; DNA: 162450 BP.
XX
AC 286967:
XX
DT 16-MAY-2000 (first entry)
XX
DE Retinoblastoma binding protein-7 genomic DNA sequence.
XX
KW RBP-7; retinoblastoma binding protein-7; abnormal cell proliferation;
XX diagnosis; therapy; cell differentiation; thyroid hyperplasia; psoriasis;
XX benign prostate hypertrophy; cancer; sarcoma; neoplasm; leukaemia;
XX lymphoma; ds.
XX
OS Homo sapiens.
XX
PN WO20000607-A1.
XX
PD 06-JAN-2000.
XX
PF 30-JUN-1999; 99WO-IB01242.
```

PR 30-JUN-1998: 98US-0091315.
PR 10-DEC-1998: 98US-0111909.
XX
PA (GEST) GENSET.
PI Bougueleret L;
XX
XX WPI: 2000-117170/10.
DR
XX
PT Novel nucleic acid and polymorphic markers used for diagnosis of
PT diseases, especially those involving abnormal cell proliferation and
PT differentiation -
XX
XX Claim 1: Page 118-163; 223pp; English.
XX
CC This sequence represents the retinoblastoma binding protein-7 (RBP-7)
CC genomic sequence of the invention. The RBP-7 coding sequence and
CC regulatory sequences are useful for the recombinant production of the
CC protein and for expressing heterologous nucleic acids. Primers and probes
CC derived from the RBP-7 nucleotide sequence (e.g. 287035-287099) are
CC useful for DNA amplification and detection methods. RBP-7 allelic
CC markers (see 286993-287034) are useful for diagnosis of disease related
CC to alteration in the regulation or in the coding regions of the RBP-7
CC gene and for prognosis/diagnosis of an eventual treatment with
CC therapeutic agents, especially agents acting on pathologies involving
CC abnormal cell proliferation and/or differentiation, these include
CC thyroid hyperplasia, psoriasis, benign prostate hypertrophy, cancers,
CC including breast cancer, sarcomas and other neoplasms, bladder cancer,
CC colon cancer, lung cancer, prostate cancer, various leukaemias, and
CC lymphomas. RBP-7 antibodies are useful as diagnostic agents.
XX
SQ Sequence 162450 BP: 45465 A; 30661 C; 32637 G; 53673 T; 14 other:

Query Match 3.3%; Score 175.2; DB 21; Length 162450;
Best Local Similarity 78.4%; Pred. No. 5.5e-30;
Matches 210; Conservative 0; Mismatches 58; Indels 0; Gaps 0;

OY 1280 aggtgagggctgtgtcttaccctacgtatgtcttaccctgagctgagctgagcacc 1339
DB 141325 AGACTTCGCTCTCTTGGCCAGGCTGAGTCCGCTGCAATCTCACTTACACCAAC 141866
OY 1340 tctgctcccaaggttcaagcaattctctgctcagcctccgcggtagctgagctagac 1399
DB 141865 TCCACCTCCCGGCTTCAAGCAATCTCTGCTGCGCTCCCAATAGCTGGACTACAG 141806
OY 1400 ggcagcgcgcgcgaattcttctgtatgttagtagagatggggttcaccataaggccg 1459
DB 141805 GCACACGCCCAAGCTAATTTTGTATTATACAGAGATGGGTTTCAACCTTATGTCAG 141746
OY 1460 gctgtctctgagctcctgagctcaggtgagctcaccacccctcctctaaagtgcagg 1519
DB 141745 GCTGCTCAACCTCCTGACCTCAAGATGATCCCTGCTGCGCTCCCAAGTCTGGG 141886
OY 1520 attacagagcatgagctacccgcgcgcgcgc 1547
DB 141685 ATTACAGGTGTGAGCCACTGTGCCAGC 141658

RESULT 12
T62346/C
ID T62346 standard; DNA: 282 BP.
XX
XX T62346:
XX
XX 11-JUN-1997 (first entry)
XX
XX Consensus Alu repeat sequence.
XX
XX Bubble: interspersed repetitive element; ligation; annealing; primer;
KW PCR: polymerase chain reaction; amplification; chromosomal aberration;
XX genetic disorder; ss.
XX

OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT primer_bind 22..45
FT /*tag- a
FT /note- "binds primer 47-23 (T62347)"
FT 216..236
FT /*tag- b
FT /note- "binds either primer Alu-S (T62348) or
FT Alu-J (T62349)"
FT primer_bind 263..282
FT /*tag- c
FT /note- "binds primer Alu-end (T62350)"
XX
XX US597694-A.
XX
XX 28-JAN-1997.
XX
XX 07-OCR-1993: 93US-0133629.
XX
XX 07-OCR-1993: 93US-0133629.
PR (MAST) MASSACHUSETTS INST TECHNOLOGY.
XX
XX Housman DE, Munroe DJ;
XX
XX WPI: 1997-108321/10.
XX
XX Amplification of nucleic acid having interspersed repetitive element
XX - using bubble oligo:nucleotide
XX
XX Disclosure: Column 19-20; 16pp; English.
XX
XX The invention relates to the amplification of region of DNA containing
XX interspersed repetitive elements (IRE) such as the Alu repeat sequence
XX presented here. The method involves ligating a double stranded DNA
XX structure with a non-complementary region, a 'bubble', in the
XX centre (e.g. see T62343-4), to restriction digested fragments of regions
XX containing IREs. The ligation results in a double stranded DNA molecule
XX containing at least one 'bubble' at either end. After denaturing the
XX structure, amplification of the IRE-containing region proceeds by PCR
XX using primers targeted to the IRE sequence (e.g. see T62347-50) and to
XX the sequence in the 'bubble' region (e.g. see T62345). The method can
XX be used to detect the presence or absence of a chromosomal aberration
XX e.g. in a genetic disorder, in a test organism.
XX
SQ Sequence 282 BP: 63 A; 75 C; 90 G; 48 T; 6 other:

Query Match 3.3%; Score 174.2; DB 18; Length 282;
Best Local Similarity 78.7%; Pred. No. 6.4e-31;
Matches 218; Conservative 4; Mismatches 47; Indels 8; Gaps 1;

OY 1280 aggtgagggctgtgtcttaccctacgtatgtcttaccctgagctgagctgagcacc 1339
DB 277 RGAATCTTCTCTGCTTCCAGGCTGAGTGCAGTGCAGATCWCAGCTCACTGTCARCC 218
OY 1340 tctgctcccaaggttcaagcaattctctgctcagcctccgcggtagctgagctgagcacc 1399
DB 217 TCCACCTCTCTGCTTCAAGGATTCCTCTGCTGAGCTCCAGATGAGTGGGATTACAG 158
OY 1400 ggc-----caagcgcgcgcgaattcttctgtatgttagtagagatggggttcaccata 1451
DB 157 GCGGCGCCCAACACAGCCCGGCTAATTTTGTATTATAGTAGAGACGGGTTTCACATG 98
OY 1452 ttagccggctgtgtcttgaacctctgacctcaggtgagctcaccacacctcagctcctaa 1511
DB 97 TTGGCCAGGCTGTGATCTGACCTCTGACCTCAGGTGATCCACCACCTCGGCTCCCAA 38
OY 1512 gtgctgagattacagcatgagctacccgcgcgcgcgc 1548
DB 37 GTGCTGGATTACAGGTGTGAGCCACCGCCAGCC 1

| | |
|----------|---|
| RESULT | 13 |
| 044278/c | ID |
| 044278 | standard: DNA: 17327 BP. |
| XX | |
| AC | 044278; |
| XX | |
| DT | 24-NOV-1993 (first entry) |
| XX | |
| DE | Serglycin - proteoglycan peptide core. |
| XX | |
| KM | Hemtopoietic cell secretory granule proteoglycan; |
| KM | positive; negative; transcriptional regulatory element; |
| KM | enhancer; eukaryotic promoter; constitutive suppressor; |
| KM | TATA-box: ss. |
| XX | |
| OS | Homo sapiens. |
| XX | |
| FH | Key |
| FH | Location/Qualifiers |
| FT | misc_signal |
| FT | 373..621 |
| FT | /*tag= a |
| FT | /note= "5' regulatory region; |
| FT | claim 1-3, page 78" |
| FT | |
| FT | 373..433 |
| FT | /*tag= b |
| FT | /note= "negative transcriptional regulatory element; |
| FT | claim 6 and 9-10, page 78-79" |
| FT | |
| FT | 514..541 |
| FT | /*tag= c |
| FT | /note= "enhancer transcriptional regulatory element |
| FT | claim 11 and 14-15, page 79" |
| FT | |
| FT | 582..602 |
| FT | /*tag= d |
| FT | /note= "eukaryotic promoter element; |
| FT | claim 16 and 19-20, page 80" |
| FT | |
| FT | 675..16646 |
| FT | /*tag= e |
| FT | /label= serglycin |
| FT | 622..753 |
| FT | |
| FT | /*tag= f |
| FT | /number= 1 |
| FT | 9597..9744 |
| FT | /*tag= g |
| FT | /number= 2 |
| FT | 16397..17327 |
| FT | /*tag= h |
| FT | /number= 1 |
| FT | 675..9598 |
| FT | /*tag= i |
| FT | /note= "interrupted by exon 1" |
| FT | 16449..16502 |
| FT | /*tag= j |
| FT | /note= "serine-glycine rich glycosaminoglycan |
| FT | attachment region" |
| FT | |
| FT | polya_signal |
| FT | 17062..17067 |
| FT | /*tag= k |
| FT | misc_difference |
| FT | 6135 |
| FT | /*tag= l |
| FT | /note= "base represented as N in the specification" |
| FT | |
| XX | |
| PN | W09313119-A. |
| XX | |
| PD | 08-JUL-1993. |
| XX | |
| PF | 23-DEC-1992; |
| XX | 92WO-US11194. |
| XX | |
| XX | 03-JAN-1992; |
| PR | 92US-0816289. |
| XX | 02-JUL-1992; |
| XX | 92US-0906871. |
| XX | |
| PA | (BGHM) BRIGHM & WOMENS HOSPITAL. |
| XX | |
| P1 | Avraham S, Stevens RL; |
| XX | |

| Query Match | Best Local Similarity | 3.3% | Score 173.6 | DB 14 | Length 17327 |
|----------------|---|------|---------------|----------|--------------|
| Matches 227 | Conservative | 0 | Mismatches 59 | Indels 8 | Gaps 1 |
| Qy 1321 | accctgagctcaactgcaacctctgctcccaaggttcaagcaattctctgctcagctcc | 1380 | | | |
| Db 7766 | atctgcgcctcaactgcaacctctgctcccaaggttcaagcaattctctgctcagctcc | 7707 | | | |
| Qy 1381 | cgctgagctggaacaaaggcgcaagc-----cgcgctcaatttggtagttgtaata | 1432 | | | |
| Db 7706 | cgagtagctggcgaacaaaggcgcaagc-----cgcgctcaatttggtagttgtaata | 7647 | | | |
| Qy 1433 | gagatgggggtttaccacatatagcccgctgctgttgaactctgaactcgaagtgatcca | 1492 | | | |
| Db 7646 | gggatgggggtttaccacatatagcccgctgctgttgaactctgaactcgaagtgatcca | 7587 | | | |
| Qy 1493 | ccacactcagcctccctaaagtgtgtggaattacaagcatgagttcacccgcccgaagg | 1552 | | | |
| Db 7586 | cccgctcagctgctcccaaaagctgctggattacagctgtagagccacacacccggcgaaa | 7527 | | | |
| Qy 1553 | gtcagtggttcaataagaataacttgaattgttacctaaaccaacagggaaaca | 1606 | | | |
| Db 7526 | gtaactttttatgaaaagacaatgtggcattgttagaaaaaacctatattcttataaaa | 7473 | | | |
| RESULT 14 | | | | | |
| ID 223900 | standard: DNA: 49999 BP. | | | | |
| AC 223900: | | | | | |
| DT 25-JAN-2000 | (first entry) | | | | |
| DE XX | Human LOBO homologue genomic DNA fragment 2. | | | | |
| DE XX | LOBO: long bones; bone development; bone extension; skull; osteopathic; | | | | |
| DE XX | diagnostic; pharmaceutical; gene therapy; transgenic animal; disease; | | | | |
| DE XX | spondyloepiphyseal dysplasia; achondroplasia; human; ds. | | | | |
| OS XX | Homo sapiens. | | | | |
| PN XX | W09950284-A2. | | | | |
| PD XX | 07-OCT-1999. | | | | |
| PF XX | 26-MAR-1999; 99WO-EP02055. | | | | |
| PR XX | 27-MAR-1998; 98DE-1013799. | | | | |
| PA XX | (ROSE/) ROSENTHAL A. | | | | |

| | | |
|----|------|---|
| XX | PI | Rosenthal A, Rump A, Hess J, Aigner T, Wirth T: |
| XX | DR | WPI: 1999-601320/51. |
| XX | PT | Nucleic acids encoding and studying which influence bone development, |
| XX | PT | useful for treating and studying bone disorders - |
| XX | XX | Example 3; Page 244-271; 391pp: German. |
| XX | PS | This invention describes novel nucleic acids (1: designated LOBO (long |
| CC | CC | bones)) encoding proteins influencing bone development in mammals. The |
| CC | CC | proteins of the invention reduce and/or inactivate bone extension (i.e. |
| CC | CC | development), with exception of the skull and have osteopathic activity. |
| CC | CC | The nucleic acid molecules, proteins and antibodies can be used in |
| CC | CC | diagnostic or pharmaceutical compounds e.g. for gene therapy. The methods |
| CC | CC | and nucleic acid molecules, etc. are useful for production of transgenic |
| CC | CC | animals, especially a transgenic mouse for the study of diseases |
| CC | CC | associated with bone development, e.g. spondyloepiphyseal dysplasia and |
| CC | CC | achondroplasia. This sequence encodes a human LOBO protein described |
| CC | CC | in the method of the invention. |
| XX | SO | Sequence 49999 BP: 11432 A; 13017 C; 12505 G; 13045 T; 0 other; |
| XX | XX | |
| XX | XX | Query Match 3.3%; Score 173.2; DB 20; Length 49999; |
| XX | XX | Best Local Similarity 81.0%; Pred. No. 9.7e-30; |
| XX | XX | Matches 217; Conservative 0; Mismatches 43; Indels 8; Gaps 1 |
| OY | 1360 | caaccgtacgtcactgaacctctgctcccgaggttaagcaattctcgtctcaagctc 1379 |
| DB | 3991 | catcttgctcactctgaacctcgcctcttggtttcaagcagatctccgctcagcc 4050 |
| OY | 1380 | ccgcgtacgtcgggactacagcg-----cagcgccggctaattttgtatgttagt 1431 |
| DB | 4051 | ccgagtagctggatatacagtgccgcgcacacagccagccagctaatttgtatttagt 4110 |
| OY | 1432 | agagatgggggtttcaacatatagccggctgtgcttgaaacctcgaactcaggtatcc 1491 |
| DB | 4111 | agagatgggggtttccacatgctggccagagctgacttgaaacctcgaactcaggtatcc 4170 |
| OY | 1492 | accgccctacagcctcctaagagtcgtgggtttcagagcatgagttacacggcgccgacag 1551 |
| DB | 4171 | acctgccttgagcctcccaagaagtgaagggttttaaggcatgagcaccagcgccacgcaag 4230 |
| OY | 1552 | gttcagtgcttaataagaataacttga 1579 |
| DB | 4231 | aagagatttataagcctattctttaa 4258 |
| XX | XX | |
| XX | XX | RESULT 15 |
| XX | XX | T42809/c |
| XX | XX | T42809 standard; DNA: 452 BP. |
| XX | XX | T42809: |
| XX | XX | 04-SEP-1997 (first entry) |
| XX | DE | Polymorphic locus 0560 sequence. |
| XX | XX | |
| KW | KW | Primer: PCR; polymerase chain reaction; amplification; polymorphism; |
| KW | KW | genomic locus; gene mapping; paternity; maternity; children; |
| KW | KW | forensic science; fingerprinting; ss. |
| XX | XX | |
| OS | OS | Homo sapiens. |
| XX | XX | |
| XX | XX | Key Location/Qualifiers |
| XX | XX | FT misc_feature 15..23 |
| XX | XX | FT /tag= a |
| XX | XX | FT /note= "sequence contains between 3-9 undefined |
| XX | XX | FT repeat_region 27..74 |
| XX | XX | FT /tag= b |

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FT FT /note= "this specification discloses that the repeat unit
FT FT TAA (bases 27-30; see below) is repeated 7-12
FT FT times; this sequence contains 12 repeats of the
FT FT TAA sequence"
FT FT
FT FT repeat_unit      27..30
FT FT /tag= c
FT FT /note= "repeated 7-12 times; this sequence contains 12
FT FT repeats of this sequence"
FT FT
FT FT repeat_unit      77..359
FT FT /tag= d
FT FT /rpt_type= Alu repeat
FT FT misc_feature      424..432
FT FT /tag= e
FT FT /note= "sequence contains between 3-9 undefined
FT FT nucleotides in this region"
FT FT
XX PN WO9634979-A2.
XX PD
XX PD 07-NOV-1996.
XX PF
XX PR 01-MAY-1996; 96MO-CA00275.
XX PR 01-MAY-1995; 95US-0432023.
XX PA (REHO-) CENT RECH HOPITAL SAINTE-JUSTINE.
XX PI Labuda D, Melancon SB, Tang JQ, Vanasse M;
XX DR WPI: 1996-506179/50.
XX XX
XX PT DNA amplification primer pair - used for simultaneous amplification
XX PT of multiple highly polymorphic genomic loci, partic. for
XX PT fingerprinting
XX PS Example 1; Fig 1; 23bp; English.
XX XX
CC CC This is the sequence of the highly polymorphic locus O560 which is
CC amplified by the primer pair R14B64/O560mak (T42806-7). The primers
CC also simultaneously amplify the loci Q900 (T42808) and Q120 (T42810).
CC The primers can be used for gene mapping, to assess paternity, maternity
CC and identity of children or in forensic science. In particular, they can
CC be used for the DNA fingerprinting identification of genetically related
CC or unrelated individuals.
XX XX
SQ Sequence 452 BP; 149 A; 92 C; 106 G; 85 T; 20 other:
Query Match 3.3%; Score 172.8; DB 17: Length 452;
Best Local Similarity 86.4%; Pred. No. 1.6e-30;
Matches 204; Conservative 1; Mismatches 23; Indels 8; Gaps 1
OY 1321 acctgagctcactgcgaacctctgctcccaaggttcaagaatctctctcgaactcc 1380
DB 312 ACTGAGCTCAGTCGAACACTGTGCCTCCAGGTTCAAGCATCTCGCTCAGCTCC 253
OY 1381 gcgcgtacgtgggaactacaaggcg-----caagcccgagctaatttttgatgttaagta 1432
DB 252 CCATTAGCTGGGATTAACAGTGCTCCGCCACCATGCCCCGGCTAATTTTGTATTTTAGTA 193
OY 1433 ggaatggaggttcacacatatagcccgagtgtgtcttgaactccctgaaccataagttatcca 1492
DB 192 GAGAGCGGGGTTTACCACGCTTGCGCAGGCTGGTCTTAAACTCTGCTCAGGTGATCTG 133
OY 1493 ccacactcagcctcctaaagtctggaattacagcatgatgcacgcgccgcggc 1548
DB 132 CCCGCTCAGCTCCCAAGAAGTCTGGGATTACAGGATAGCACACC GCCCGGCC 77

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